



FIG. 1A

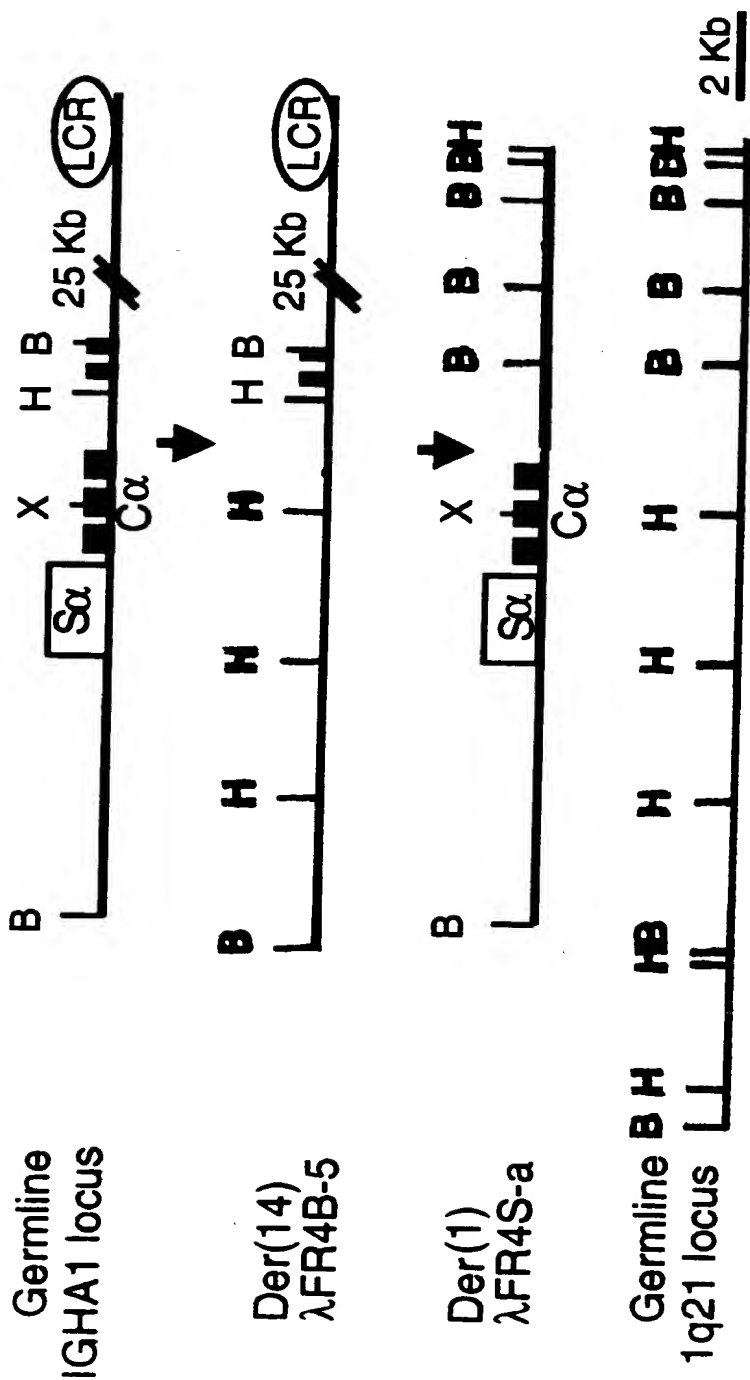


FIG. 1B

Chr 1 GGGCCTGACAGCAACTTTTCTTCTACTACTAGTTTCATCTTAAC
|||||
der14 GGGCCTGACAGCAACTTTTCTTCTACTACTAGTTTCATCTTAAC
Chr 14 TCCCCTGACGCATGCAGGAAGGGCACCTCCCCCTTAACC

FIG. 1BA

TTTATCCTGGTAACTGGCGGAGACAACCTGTCTTAAGTAACTGAAGGAAA
ACACTGCTCTGTACGGGGCACCGTGGGCACAGGTGCACACTCACACTCACA
|||||
ACACTGCTCTGTACGGGGCACCGTGGGCACAGGTGCACACTCACACTCACA

FIGURE 2A

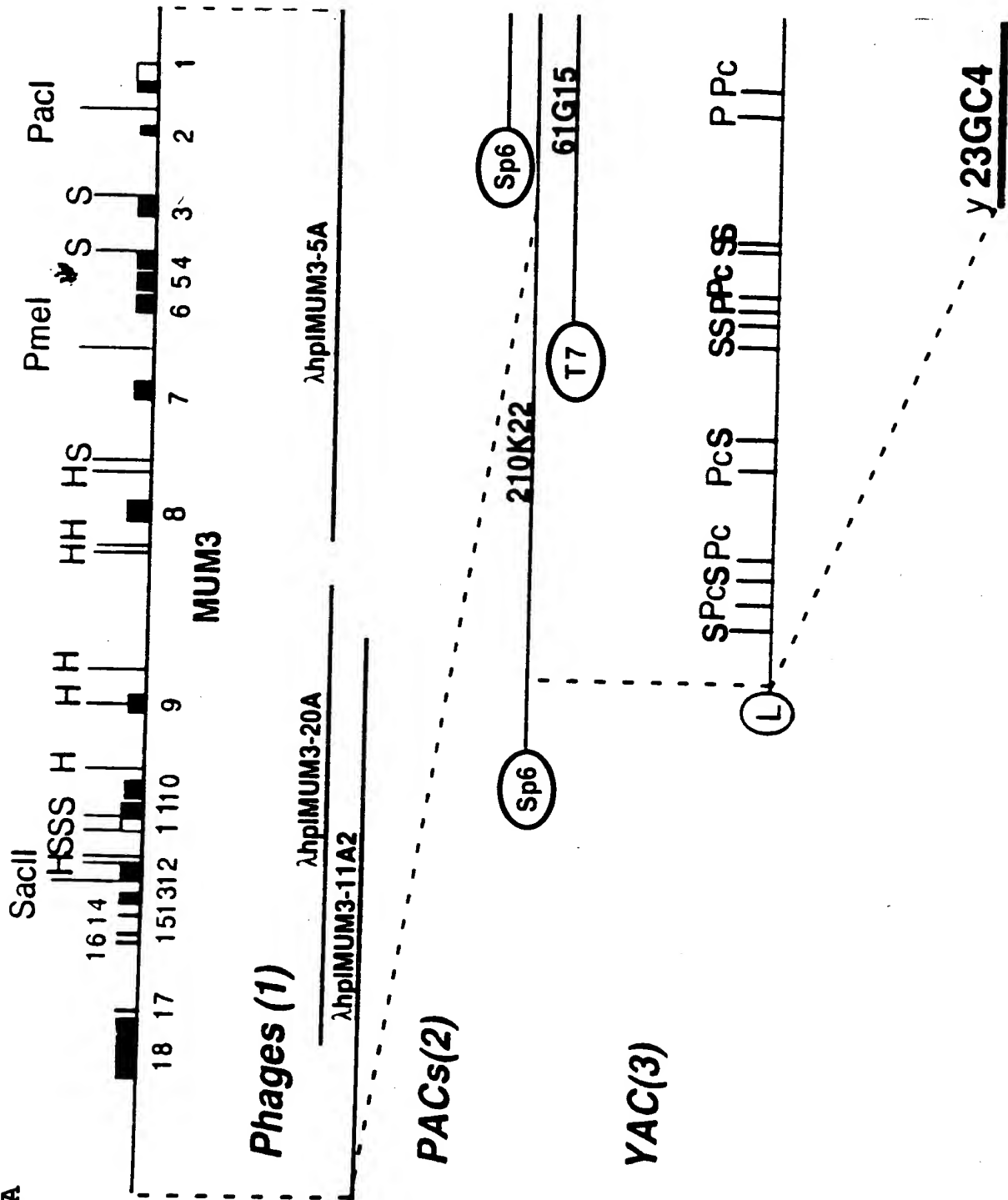


FIGURE 2AA

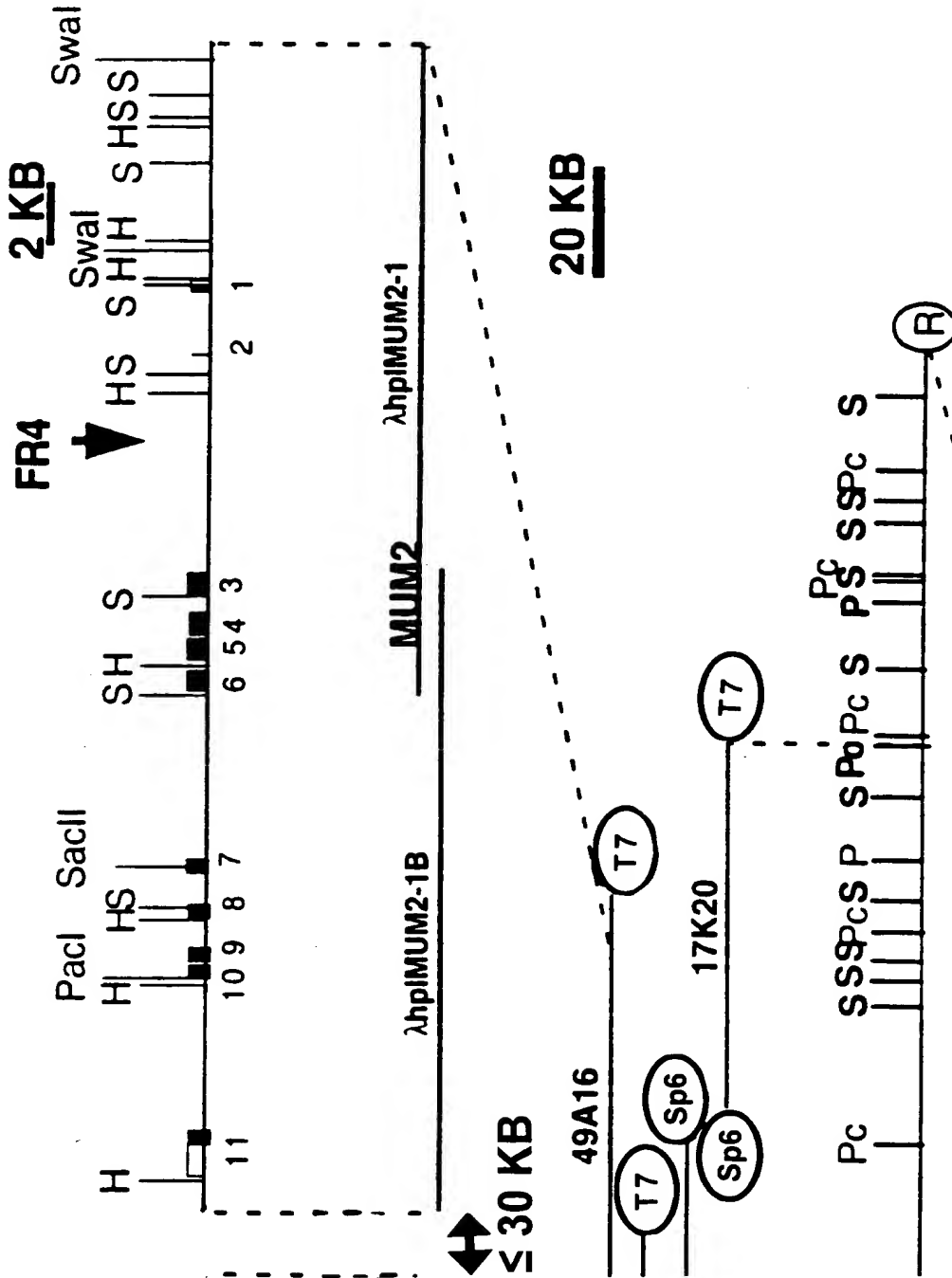
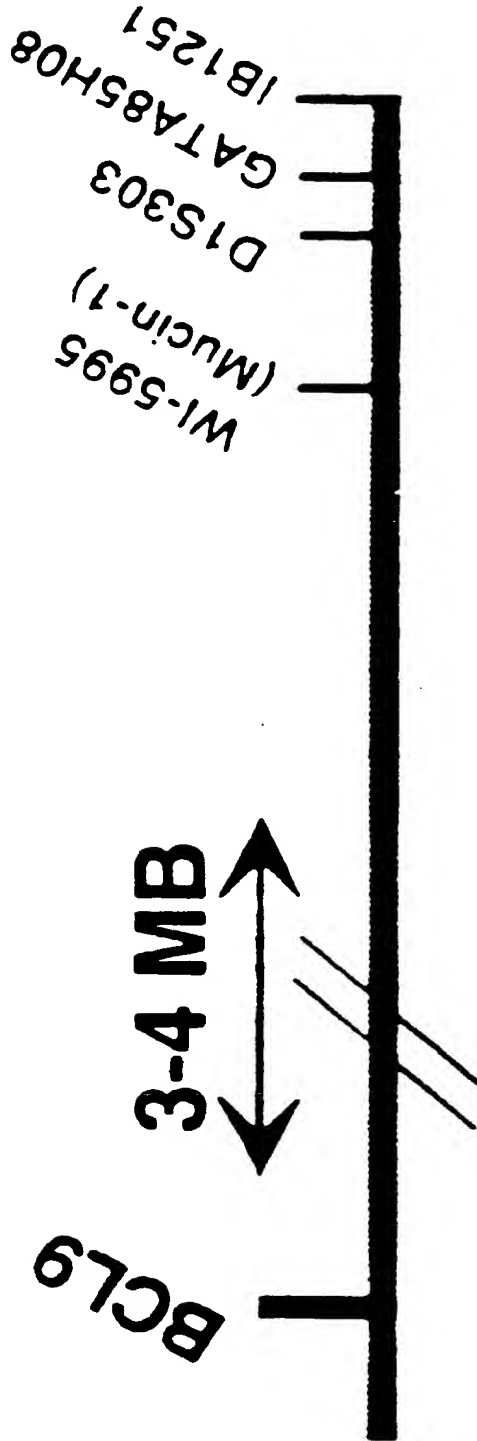


FIGURE 2B

CEN



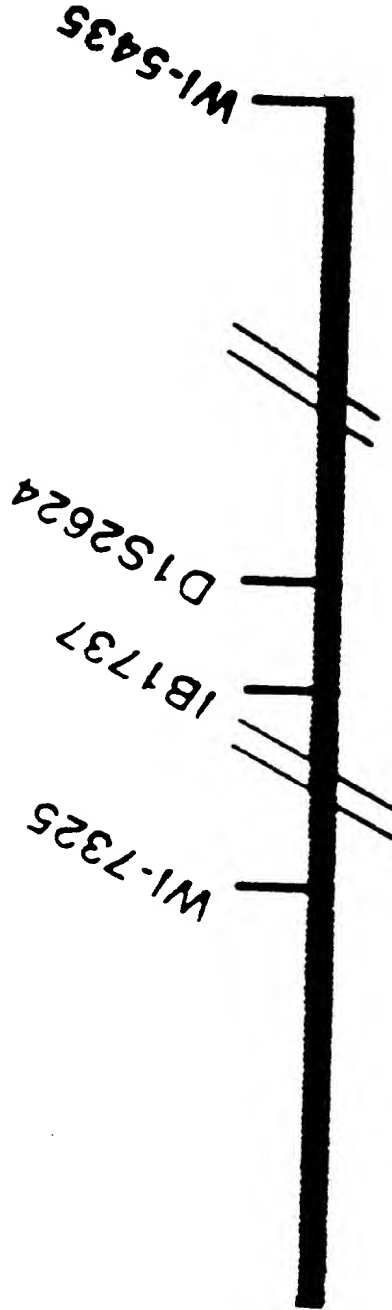


FIGURE 2BA

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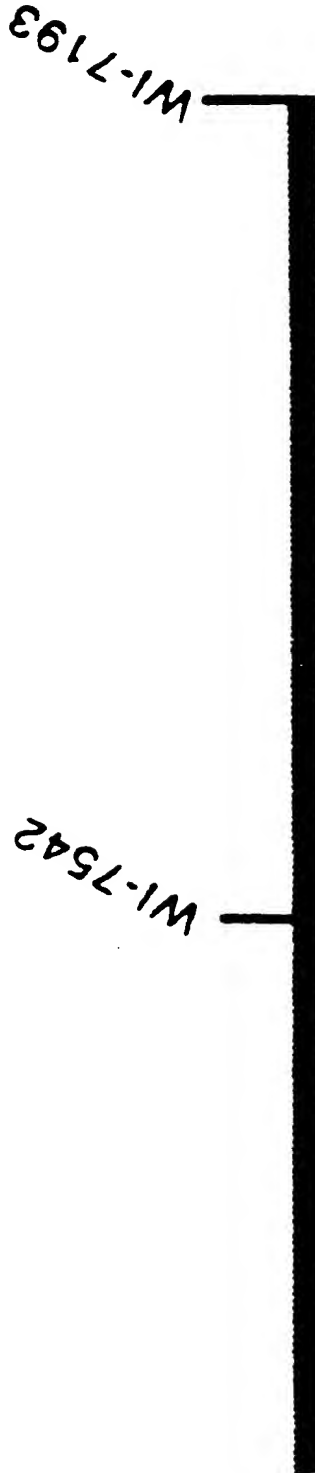


FIGURE 2BB

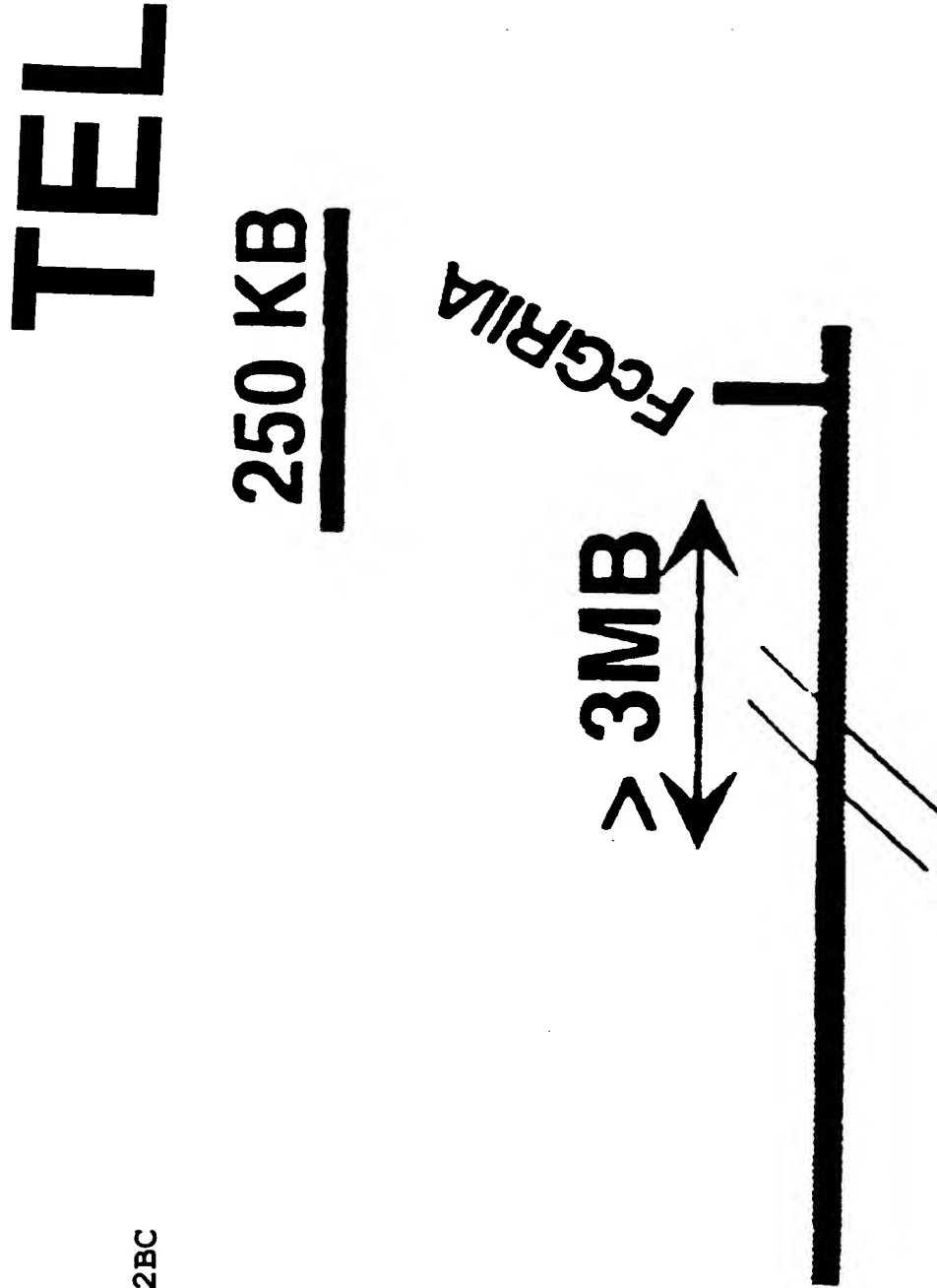
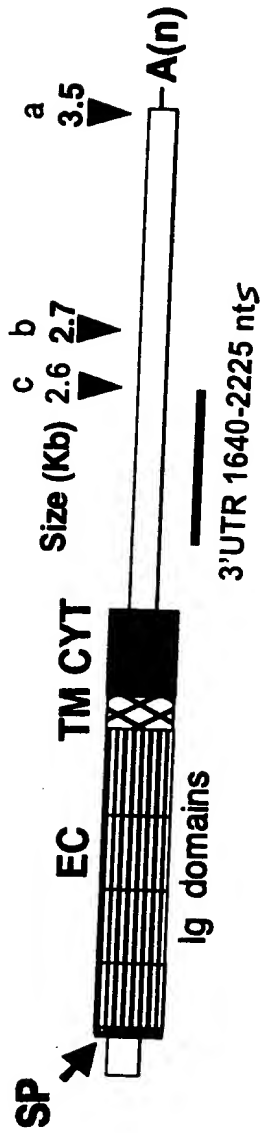


FIGURE 2BC

FIG. 3A



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FIG. 3B

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FIG. 3C

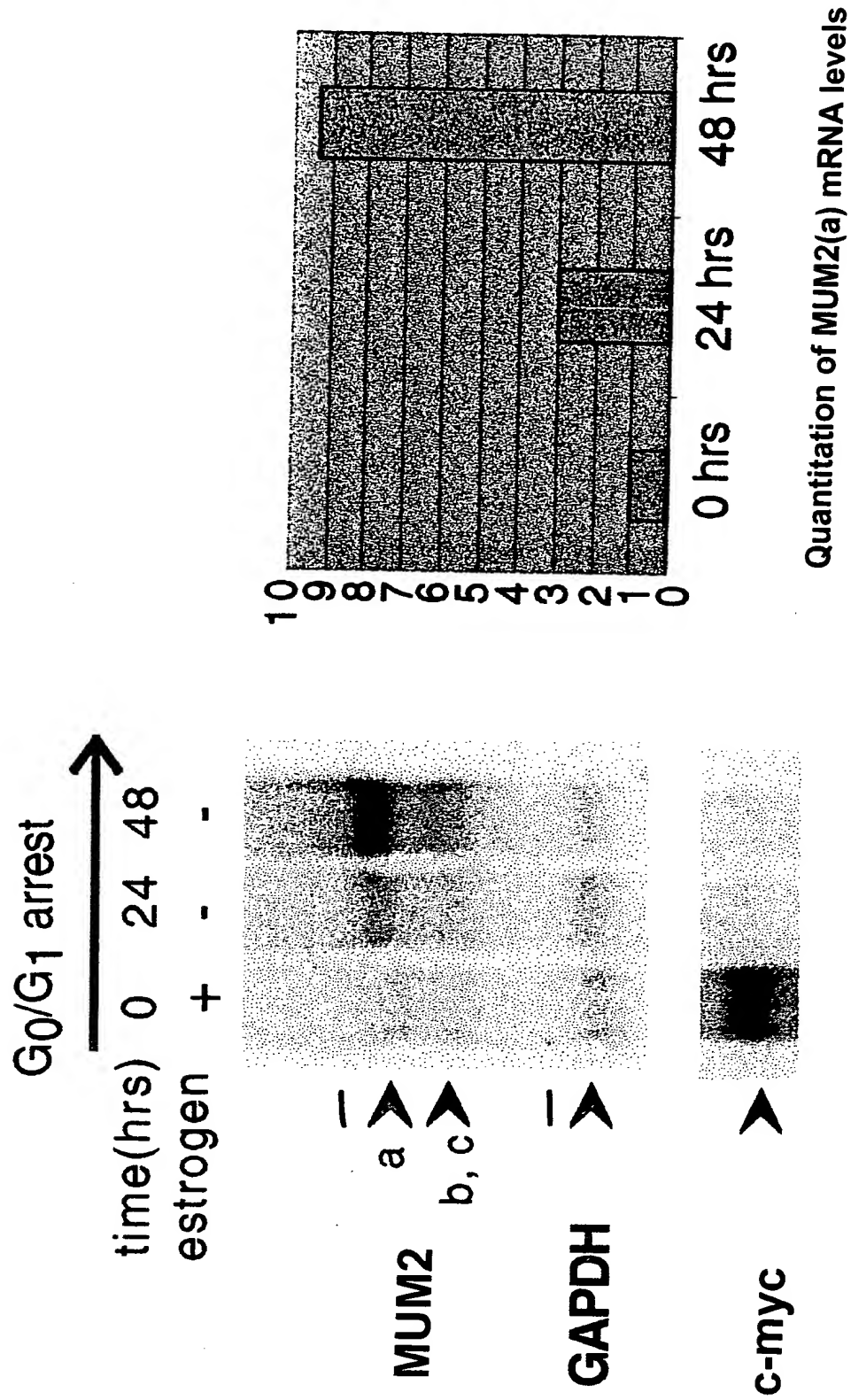
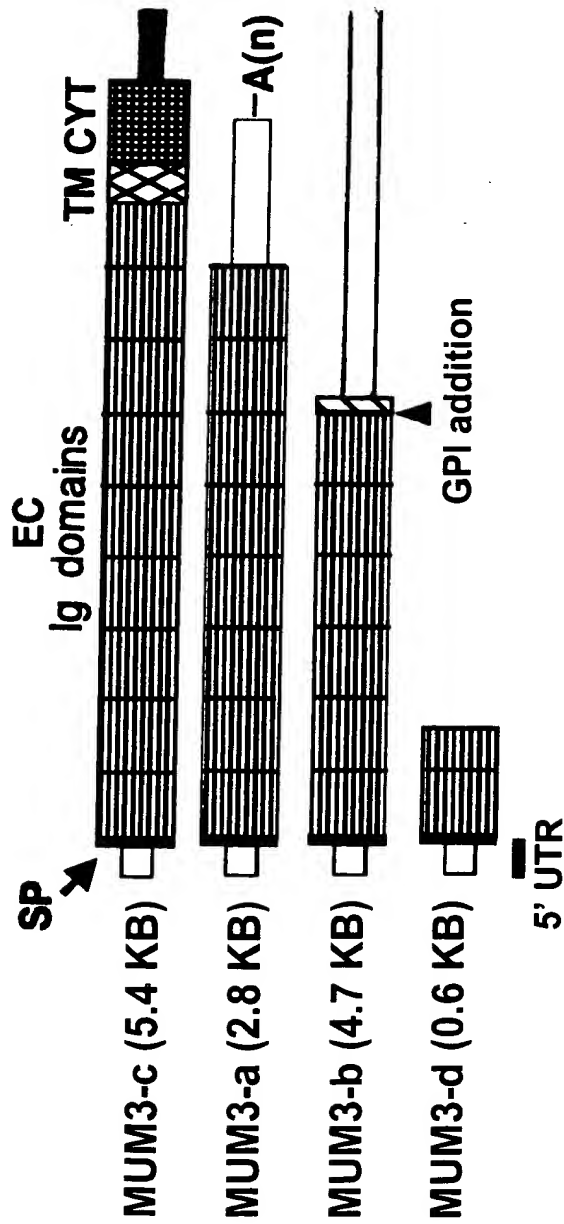
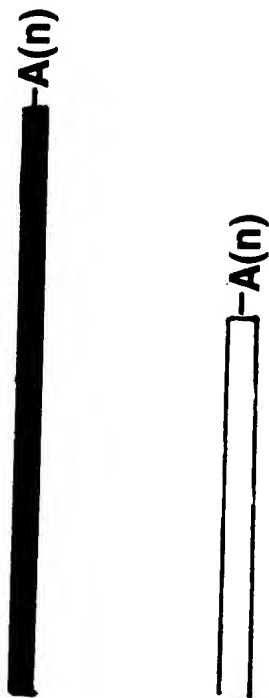


FIG. 4A

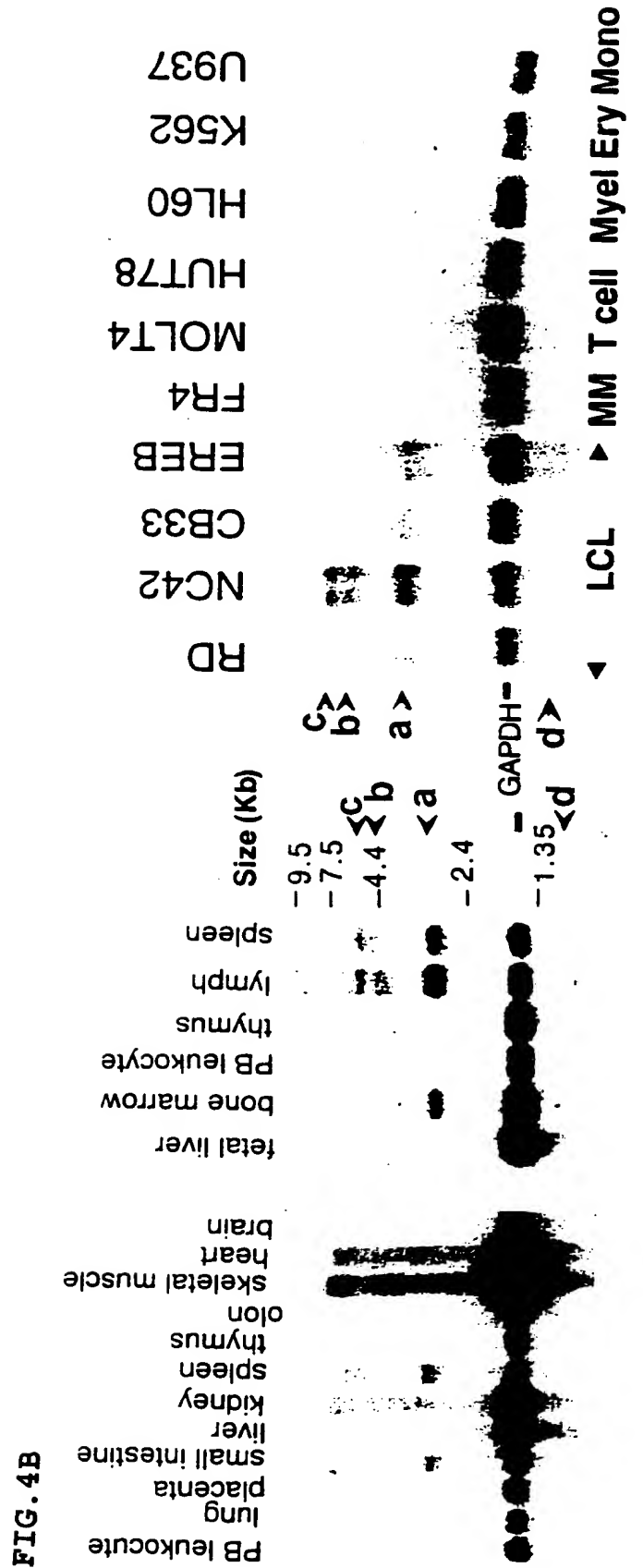


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FIG. 4AA



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FIGURE 5

1 CTCAATCAGCTTTATGCAGAGAAGAAGCTTACTGAGCTCACTGCTGGTGGTGGTAGGCAAGTGTCTTTGGCAA
 78 TCTGGGCTGACCTGGCTTGTCTCTCAGAACTCCTTCTCAACCTGGAGCAGGCTTCCATGCTGTGGCGTCC
 155 L L A F A P V C G Q S A A A H K P V I S V H P P W T 32
 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGCAGCTGCACACAACTGTGATTTCCGTCATCCTCCATGGAC
 232 T F F K G E R V T L T C N G F Q F Y A T E K T T W Y 58
 CACATTCTTCAAAGGAGAGAGTGAATCTGACTTGAATGGATTTCACTTCTATGCAACAGAGAAACAACATGGT
 309 H R H Y W G E K L T L T P G N T L E V R E S G L Y 83
 ATCATCGGCACACTACTGGGGAGAAAGTTGACCTTGACCCAGGAACACCCCTCGAGGTTCCGGAATCTGGACTGTAC
 386 R C Q A R G S P R S N P V R L L F S S D S L I L Q A 109
 AGATGCCAGGCCCGGGCTCCCCACGAAGTAACCTGTGCGCTTGTCTTTCTTCAGACTCCTTTAATCCTGCAGGC
 463 P Y S V F E G D T L V L R C H R R K E K L T A V K 135
 ACCATATTCTGTGTTGAAGGTGACACATTGGTTCTGAGATGCCACAGAAGGAAGAAATTGACTGCTGTGA
 540 Y T W N G N I L S I S N K S W D L L I P Q A S S N 160
 AATATACTTGAATGGAACATTTCTTCCATTTCTAATAAAGCTGGGATCTTCTATCCACAAAGCAAGTTCAAT
 617 N N G N Y R C I G Y G D E N D V F R S N F K I K I 186
 AACATGGCAATTATCGATGTCATGGATATGGAGATGAGAATGATGTATTAGATCAAAATTTCAAAATAATTAAT
 694 Q E L F P H P E L K A T D S Q P T E G N S V N L S C 212
 TCAAGAACTATTTCACATCCAGAGCTGAAAGCTACAGACTCTCAGCTACAGAGGGGAATTTGTAAACCTGAGCT
 771 E T Q L P P E R S D T P L H F N F R D G E V I L 237
 GTGAACACAGCTTCTCCAGAGCGGTCCAGACACCCCACTTCACTTCAACTTCTTCAGAGATGGCGAGGTCACTCTG
 848 S D W S T Y P E L Q L P T V W R E N S G S Y W C G A 263
 TCAGACTGGAGCACGTACCCGGAATCCAGCTCCCAACCGTCTGGAGAGAAACTCAGGATCCTATTGGTGTGGTGC
 925 E T V R G N I H K H S P S L Q I H V Q R I P V S G V 289
 TGAACACAGTGAAGGTAACATCCACAAAGCACAGTCCCTCGCTACAGATCCATGTGCAGCGGATCCCTGTCTGGGG
 1002 L L E T Q P S G G Q A V E G E M L V L V C S V A E 314
 TGCTCTGGAGACCCAGCCCTCAGGGGCCAGGCTGTGAAGGGAGATGCTGTGCTCTGTCTCGTGGCTGAA
 1079 G T G D T T F S W H R E D M Q E S L G R K T Q R S L 340
 GGCACAGGGGATACCACATTCTCTGGCACCGAGAGGACATGCAGGAGAGTCTGGGGAGGAAACTCAGCGTTCCCT
 1156 R A E L E L P A I R Q S H A G G Y Y C T A D N S Y G 366
 GAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGAGCCCATGCAGGGGGATCTACTGTACAGCAGACAAACAGCTACG
 P V Q S M V L N V T V R E T P G N R D G L V A A G 391

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FIGURE 5A

1233 GCCCTGTCCAGAGCATGGTGTGAATGTCACTGTGAGAGAGACCCAGGCAACAGAGATGGCCTTGTCCGCCGGGA
1310 A T G G L L S A L L L A V A L L F H C W R R R K S G 417
GCCACTGGAGGGCTGCTCAGTGTCTTCTCCTGGCTGTGGCCCTGCTGTCTCACTGTGGCTGGAGGAGTCAGG
1387 V G F L G D E T R L P P A P G P G E S S H S I C P A 443
AGTTGGTTTCTTGGGAGACGAACCCAGGCTCCCTCCGCTCCAGGCCCCAGGAGAGTCTCCCATTCCTGTCCTG
Q V E L Q S L Y V D V H P K K G D L V X S E I Q T 468
1464 CCCAGGTGGAGCTTCAGTGTGTGATGTATGATGTACACCCCAAAAGGGAGATTGTTGTTATCTCTGAGATCCAGACT
T Q L G E E E A N T S R T L L E D K D V S V Y S 494
1541 ACTCAGCTGGGAGAGAGAGGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTC
E V K T Q H P D N S A G K I S S K D E S * 515
1618 TGAGGTAAAGACACACACCCAGATAACTCAGCTGGAAGATCAGCTCTAAGGATGAAGAAAGTTAAGAGAAATGAAA
1695 AGTTACGGGAACGTCCTACTCATGTGATTTCTCCCTTGTCCAAAGTCCAGGCCAGTGCAGTCTTGGGGCACCTG
1772 GAATGATCAACTCATTCAGCTTTCTAATTTCTCATGTCATATGCATTCACTCCAGGAATACTCATTCGTCTACT
1849 CTGATGTTGGGATGGAATGGCTCTGAAAGACTTCACATAAATGACCAGGATCCACAGTTAAGAGAAAGACCCCTGTAG
1926 TATTTGCTGTGGCCCTGACCTAATGCATTCCTAGGCTGTGCTTTAGAGAGGGGGATGAAGAGAGAGAGAGGACTGT
2003 TATGAAAACAGAGACACAAATTTTGGTGAAATTTGGGATTTGCAGAGATGAAAAGACTGGGTGACCTGGATCTCTGC
2080 TTAATACATCTACAAACCATTTGCTCACTGGAGACTCACTTGCATCAGTTTGTAACTGTGAGTGGCTGCACAGGCA
2157 CTGTGCAACAATGAAAAGCCCTTCACTTCTGCTGCACAGCTTACACTGTCAAGGATTCAGTTGCAGATTAAAGAA
2234 CCCATCTGGAATGTTTACAGAGAGAGGAATTTAAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
2311 GCTTCCAAAGCAAAATGATAATTAATGTTAATGTCAATAGTGACAAAGATTTGCCAACATTAGAGAAAAGAGACACAAA
2388 TATAAAATTAAAAAATTAAGTACCAACTCTCCAAAACCTAAATTTGAACTTAAATATTAGTATAAACTCATAATAA
2465 CTCTGCCTTTAAATAAAAAAATAAAAAA

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FIGURE 6a

1 CCGTGCAGTGTCTGACTGTAGATCAAGTCCAAACCTGTTTGGAAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTG
 81 GTGGTCCAGGCTTCAATGCTGTGGGTGATATTACTGGTCTGGCTCCTGTCTAGTGGACAGTTTGCAGGACACCCAG
 161 GCCCATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAGGAGAGAGAGTGTACCCCTCACTTGAAGGATTTTCGCT
 241 TCTACTCACCACAGAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCACAGACAATATCCTT
 321 GAGGTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGCTCCCTCTCTCAGTAGCCCTGTGCACCTTGGATTTTCTTC
 401 AGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGGTCTGAGGTGCCGGCAAGCGGAAG
 481 TAACACTGAATAATACTATTACAAGAATGATAATGTCTCGCATTCCTTAATAAAGAACTGACTTCCATATTCCTCAT
 561 GCATGTCTCAAGGACAAATGGTGCATATCGTGTACTGGATATAAGGAAGTTGTTGCCCTGTTTCTTCCAATACAGTCAA
 641 AATCCAAGTCCAAGAGCCATTTACACGTCAGTGCTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
 721 TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTCAGATGTCCCGCTCCGGTTCGCTTCTTCCAGAGATGACCAGACCCCTG
 801 GGATTAGGCTGGAGTCTCTCCCGAATTTCCAGATTACTGCCATGTGGAGTAAAGATTTCAGGGTTCTACTGGTGTAAAGGC
 881 AGCAACAATGCCTCACAGCGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC
 961 TCACCTCAGCCCTGAAAGGCTCTGAATTTGAGGGAACCAAGGTGACACTTCACTGTGAACCCAGGAAGATTCTCTG
 1041 CGCACTTTGTACAGGTTTATCATGAGGGTGTCCCTCCCTGAGGCACAAAGTCAGTCCGCTGTGAAGGGGAGCATCCATCAG
 1121 CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACATGGCCCTTGGGCCAAGCCAGTAAAGGCTG
 1201 TGAGCCTCTCAGTCACTGTTCGGGTCTCATCTCTCAACCTCAGCTCTCCTGAGGACCTGATTTTGGAGGAGCC
 K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E 422

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FIGURE 6aA

1281 AAGTGACACTTCACTGTGAAGCCACAGAGAGGTTTCACTCCCATCTCTGTACCAGTTTCATCATGAGGATGCTGCCCTGGA
 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T449
 1361 GCGTAGGTGGCCAACTCTGCAGGAGGAGTGCCCATCAGCTTCTCTGACTCCAGAGCATTCAGGGAATCTACTGCA
 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
 1441 CAGTGACAATGGCTTTGGCCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCAGTGTCCCTGTCTCATCTCTGTCTC
 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
 1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACA
 I L Y Q F Y H E D M P L W S S T P S V G R V S F S F529
 1601 AATCCTATACCAGTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTCTCAGCT
 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
 1681 TCTCTGACTGAAGGACATTCAGGGAATTAATACTGACAGCTGACAATGGCTTTGGTCCCGAGCGCAGTGAAGTGGTG
 S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582
 1761 AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCCATCTCACCTCAGGGTTCCCGAGGCCAGGCTGTGGTGGGGACCT
 L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609
 1841 GCTGGAGCTTCACTGTGAGGCCCGAGAGGCTCTCCCCAATCCTGTACTGGTTTATCATGAGGATGTACCCCTGGGA
 S S A P S G G E A S F N L S L T A E H S G N Y S C E 635
 1921 GCAGCTCAGCCCCCTCTGGAGGAGAGCTTCTTTCAACCTCTCTGACTGCAGAACATTTCTGGAACTACTCATGTGAG
 A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662
 2001 GCCAACAAATGGCTAGTGGCCCGACAGTGCACACAATATCACTCAGTGTATAGTTCCAGTATCTCGTCCCATCTCAC
 F R A P R A Q A V V G D L L E L H C E A L R G S S P I689
 2081 CTTCAGGGCTCCCAGGGCCAGGCTGTGGTGGGGACCTGCTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA
 L Y W F Y H E D V T L G K I S A P S G G G A S F N L 715
 2161 TCCTGTACTGGTTTATCATGAAGATGTCACCCCTGGGTAAGATCTCAGCCCCCTCTGGAGGAGGGCCCTCCTTCAACCTC
 S L T T E H S G I Y S C E A D N G L E A Q R S E M V T 742
 2241 TCTCTGACTACAGAACATTTCTGGAATCTACTCCTGTGAGGCAGACAATGGTCTGGAGGCCCGAGCGCAGTGAGATGGTGAC
 L K V A G E W A L P T S S T S E N * 759
 2321 ACTGAAAGTTGCAGGTGAGTGGGCCCTGCCACAGCAGCACATCTGAGAACTGACTGTGCTTCTCCCTGCAGCTGA
 2401 AATGGAGCCACAGAGCTCCTCAGGGCTGTTTGTGTGGCATCCAGCACACTTCTCTGCTGCAGAACCTCCCTGTG
 2481 AAAGTCTCGGATCCTTTGTGGTATGGTTCCAGGAATCTGATGTTTCCAGCAGTCTTCTTGAAGATGATCAAGCACCTC
 2561 ACTAAAAATGCAATAAGACTTTTGTAGAACATAAATACTATATCTGAACCTGAAATATTATACATGAAATGAAACCAAGA
 2641 ATTCTGAGCATATGTTTCTGCGGTAGAAAGGATTAAGCTGTTTCTTGTCCGGATTCTTCTCTCATTTGACTTCTAAGAA
 2721 GCCTCTACTCTTGAGTCTCTTTTCATTACTGGGATGTAATGTTTCTCTTACATTTCCACATTAATAATCCTATGTTAACGA
 AAAA

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FIGURE 6b

```
1  CCGTGCACTGCTCCTGACTGTAAGATCAAGTCCAAACCGTGTGTTGGAAATGAGGAAACTTCTCTTTTGATCTCAGCCCTTG
    M L L W V I L L V L A P V S G Q F A R T P R
81  GTGGTCCAGGTCTTCATGCTGCTGGTGATATTAATGCTGCTGGCTCCTGTGACGTGACAGTTTGCAAGGACACCCCG
    P I I F L Q P P W T T V F Q G E R V T L T C K G F R F
161  GCCCATTTATTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTACCTCCTCAGTGGCAAGGATTTTCGCT
    Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L
241  TCTACTCACCAAGAAACAAATGGTACCATCGGTACCTTGGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTT
    E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S
321  GAGGTTCAGGAATCTGGAGAGTACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTTGGATTTTCTTC
    A S L I L Q A P L S V F E G D S V V L R C R A K A E V
401  AGCTTCGCTGATCCTCAAGCTCCACTTTCTGTGTTTGAAGGAGACTCTGTGTTCTGAGGTGCCGGGCAAGGCGGAAG
    T L N N T I Y K N D N V L A F L N K R T D F H I P H
481  TAACACTGAATAATACTATTACAAGAATGATAATGCTCTGGCATTCTTAATAAAGAACTGACTTCCATATTCCTCAT
    A C L K D N G A Y R C T G Y K E S C C P V S S N T V K
561  GCATGTCTCAAGGACAATGGTGATATCGCTGTACTGGATATAAGGAAAGTTGTGCCCTGTTTCTTCCAATACAGTCAA
    I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L
641  AATCCAAGTCCAAGAGCCATTTACAGTCCAGTGTGAGAGCCAGCTCCTCCAGCCCATCAGCGGGAACCCAGTGACCC
    T C E T Q L S L E R S D V P L R F R F R D D Q T L
721  TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTGATGTCGCCGTCGCTCCGTTCCGTTCTTCAGAGATGACCAACCCCTG
    G L G W S L S P N F Q I T A M W S K D S G F Y W C K A
801  GGATTAGGCTGGAGTCTCTCCCGAATTTCCAGATTAATGCCATGTGGAGTAAAGATTCAGGGTTCTACTGGTGAAGGC
    A T M P H S V I S D S P R S W I Q V Q I P A S H P V L
881  AGCAACAATGCCCTCACAGCGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCGATCCTGTCATCTCATCTGTCC
    T L S P E K A L N F E G T K V T L H C E T Q E D S L
961  TCACCTCAGCCCTGAAAAGGCTCTGAATTTTGAGGGAACCAAGGTGACACTTCACTGTGAAACCCAGGAAGATTCTCTG
    R T L Y R F Y H E G V P L R H K S V R C E R G A S I S
1041  CGCACTTTGTACAGGTTTATCATGAGGGTGTCCCTGAGGCACAGTCACTGCGCTGTGAAAGGGAGCATCCATCAG
    F S L T T E N S G N Y Y C T A D N G L G A K P S K A V
1121  CTTCTCACTGACTACAGAGAATTCAGGGAACCTACTACTGCACAGCTGACAATGGCCTTGGCCCAAGCCAGTAAGGCTG
    S L S V T V P V S H P V L N L S S P E D L I F E G A
1201  TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTCTCAACCTCAGCTCTCTGAGGACCTGATTTTGTAGGGAGCC
    K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E
1281  AAGTGACACTTCACTGTGAAGCCAGAGAGGTTCACCTCCCATCTCTGTACCAGTTTCATCATGAGGATGCTGCTCCCTGGA
```

FIGURE 6bA

1361 R R S A N S A G G V A I S F S L T A E H S G N Y Y C T 449
 GCGTAGGTCGGCCAACTCTGCAGGAGGAGTGCCATCAGCTTCTCTGACTGCAGAGCATTCAGGGAACACTACTACTGCA
 1441 A D N G F G P Q R S K A V S L S I T V P V S H P V L 475
 CAGCTGACAAATGGCTTTGGCCCCCAGCGCAGTAAGGCGTGAGCCTCTCCATCAGCTGTCCTGTCTCATCTCCTGTCCTC
 1521 T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCACACA
 1601 I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F 529
 AATCCTATACCAGTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTTCAAGCT
 1681 S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
 TCTCTGACTGAAGGACATTCAGGGAATTAATACTGACAGCTGACAAATGGCTTTGGTCCCGCCAGCGCAGTGAAGTGGTG
 1761 S L F V T G K C W V L A S H P P L A E F S L T H S F K 582
 AGCCTTTTGTCACTGGTAAGTGGTCTTGGCCAGTCACCCACCCCTGGCTGAGTCTCTCTCACCCCATTCCTTTAA
 N L F A L S S F L P * stop 592
 1841 AAATCTGTTTGCAGTGTCCAGTTTCCCTCCCTAATCACTTAATCCCTTCTTGGCTTCTCCTCAACTAAGTCTGGG
 1921 GTTTTCCGTAATAAGTCTGGCTCAGCCAGACCCCTAAACAGCTCAGTAGATTCCCGAGCTTTTACCAATGAATT
 2001 TATTTATGTATTTCTCCTCATTCCTGTATGTTCACAGTACGCCAAATTTTCTTGATGACGCGGTGTCTACT
 2081 TCTCTACTGACATTTACATATTAATCTAGCTACAGCACAGTCTTATAGATAAATATTTGGTCAAGACCTTAATTTCTCCA
 2161 AAGGATTTCCAAATCTTATGTAGATTTGGAGAAAGCTGTGGTAACAAAGGGGGAATGGCTCCCTAGGAACCAACTCC
 2241 TCAACTTCTGGAGTTTATGATCCCTGTTTCTAACCTGCTAAATCAGTATCATTTTATTTATTTTAAATAA
 2321 ACTATTGTTGAAGTATGACATACATTCAAGAAACGCTGTGCAAAATTGTATGTGTACGATTTGGTGTCTTTTAGGAGCTAA
 2401 GTTGCTTCTGTTTACTTGAATCTTTGTTTATAGAAACTGGGGGAAAGTTTACTTCTTTTTCAGAGAAGCCAAATGGTA
 2481 TGATAGAAAATCTTTGAGCCTGATGTGTGAGCATGCCCCCTAGCATAACTTTGTTGAGTAAAGAGGTTATTTTAAATGT
 2561 GAATGTTCTGAGACTACTCCAAAGTCAGAGCCAAATCTACTAGGAAGCTTCTAGACTTCACTCATTTCTGTCATCCCATTAC
 2641 TATCTTTTATCCATGTTTACTTCTTCTCATATTTCAGCAGCATCTTAAGCCTCTTATTTTCTTGTCTTGTACTGTCA
 2721 CCTTAAATGCCAGTAGAATGTAAAGCTTTCATGAGAACAGAACTGCATCCATCTTGGTCTTTCACAAACATCCCTGTGSCCTACT
 2801 CAGTGTTTGGCACACAGTAGGTCTCAGTCAACATTTGTAAATTTAGTGGACAGATGATATGACAAGATGATAGAGGGGA
 2881 TTTAAATAATCATCTAGCAAGCCCAAGAGGAAAACAAAGCTATTTTAGAATAATGAATACCAATTTGAAGCAGTA
 2961 AGAATAGATTGGATATCTTTGAAAACCATTAATTTGAATGAAGAACCAATTTTGAGAAAACAATACAGAATGCAAGTAGAA
 3041 AGATACAGAAATAAAGGCAAAAGTTATAATATGGAATCAGACAATGGATTTGTCTGTATCCAGTTATGTGGATAATTAA
 3121 AATGGAGACCTCAGAAAATTGAACCGAAGAGTAAATGAACTCAAAATGTAGTAGAATTTGTTGGGAAGTAAAGAAA
 3201 ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATTTGACTTTTGAGGTTTAAAAATATATATATGTGCTATGAT
 3281 TATGGGGAAAAAAGCAGTCGTCTCAGAAAGAAAAACATCAAGTTAGTCTTAGACTTTTGCAGTGCACCTCAGTACCCAAAGAG

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FIGURE 6bB

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3361 AGAGGAGGCCGAGACTTGGACCTGCGAGGGGAAGAAATAAACCAGAAAATTTTATATCAATTCAAAAAGACATTGTCAAAA
3441 TACAGGGATTTCAGGAAACTGAGAAATGCACCTAAGCCTTCTGGAAAAAACAACCTAATGACAAAAATCTAGCCCCAACAGATGT
3521 AAATGAATATAAAGGACTCATAATGAGGAAACCGCATTTATGACTGGCTCTCAACCTGGCCGCAATATTAGACTCGTCAAA
3601 GACCTTTGTAAAAGGTCACACATTGACTCGTCAAAAGCCCTCTCCAGACTAATTCAATTTCAGAAATCTCACAGATGGGGCC
3681 ACAGAAATCAGTATTTTGTGACACACACCTCAAGTGAGAAATATTGTGTAGACAAAGATTGGAAACCCACTGATTTAGATATAGA
3761 AACAAAGGCTAATCAACTGTGAGAAATTAATGGTCACAGAAATAGAAAGTAACCTATTATGAACACTGAATAATGTAAAAAAT
3841 GTAACAAAGAAATAATAGTTAGAGGAAGGAGAGGAAGTAAGGAACAATCATTTTCTCATGATTATTATTATTTTCAGAGTA
3921 AATTGTGAGTTATTTCACAAATTCAAAAAGAAATGGACTGTTTTTAAAAAATTAGTAATAGATTTCAAAAATGTCCATTTTGTA

4001 AATCGTTTCTGAATACTTTGTCAACAGTTACTCATCTAATTAATGGCTTATACTTCACTAAAAATTCATGGAAAAACCACTA
4081 GTAGCCTGTAGAGTCACATAGGAGAGAACAAAGTGAATTTCTTTGGGTGGCGCAAGCATAGATGTTAGGACTGACAAAAAAA
4161 AATAATAAAAAATAAACCTGTGCAATTGATATGATCACAAATGATCAGGGAAAGAGGAAACAGAAAATCTCTCATACGCCATT
4241 TTACAAGTGTAATTTGGTTCAACCTTTTCGTCCTTAATTGACACACATTGTAATTGTATATATTATGGAAGCACAGTTTGAT
4321 ATTTTGATATACATACATGGTATATAACGATCAAAATTAGGATATTTAATGTACCCCATCATCTCATGCAATTTATCATTTCT
4401 TTGGAATAAA AACATTCAA AGCCAAAAA AAAAAAAA AAAAAA
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FIGURE 6c-1

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1  CCGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTGGGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTG
    M L L W V I L L V L A P V S G Q F A R T P R
81  GTGGTCCAGGTCTTCATGCTGTGGTGATATTACTGGTCTGCTGCTGTCAGTGGACAGTTTGAAGGACACCCAG
    P I I F L Q P P W T T V F Q G E R V T L T C K G F R F
161  GCCCATTTATTTCTCCAGCCTCCATGGACCACAGTCTTCCCAAGGAGAGAGAGTGCCTCAGTTCGCAAGGGATTTCGCT
    Y S P Q K T K W Y H R Y L G K E I L R E T P D N I L
241  TCTACTCACCACAGAAACAATGTACCATCGGTACCTTGGGAAGAAATACTAAGAGAAACCCACAGACAATATCCTT
    E V Q E S G E Y R C Q A Q G S P L S S P V H L D F S S
321  GAGGTTCAGGAATCTGGAGATCAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACCTGGATTGTTCTTC
    A S L I L Q A P L S V F E G D S V V L R C R A K A E V
401  AGCTTCGCTGATCCTGCAAGCTCCACTTCTGTGTTTGAAGGAGACTCTGTGGTGTCTGAGGTGCCGGGCAAGGGCGGAAG
    T L N N T I Y K N D N V L A F L N K R T D F H I P H
481  TAACACTGAATAATACTATTACAGAATGATAATGTCTGGCATTCCTTAATAAAGAACTGACTTCCATATTCCTCAT
    A C L K D N G A Y R C T G Y K E S C C P V S S N T V K
561  GCATGTCTCAAGGACAATGGTGATATCGCTGTACTGGATATAAGGAAGTTGTGCTTCCCTGTTTCTTCCAAATACAGTCAA
    I Q V Q E P F T R P V L R A S S F Q P I S G N P V T L
641  AATCCAAGTCCAAAGAGCCATTTACACGTCACAGTGTGAGAGCCAGCTCCTTCCAGCCCATCAGCGGGAACCCAGTGACCC
    T C E T Q L S L E R S D V P L R F R F R D Q T L
721  TGACCTGTGAGACCCAGCTCTCTCTAGAGAGGTGATGTCCCGCTCCGGTTCCTTCCAGAGATGACAGACCCCTG
    G L G W S L S P N F Q I T A M W S K D S G F Y W C K A
801  GGATTAGGCTGGAGTCTCTCCCGAATTTCCAGATTACTGCCATGTGGAGTAAGATTTCAGGGTTCTACTGGTGTAAAGGC
    A T M P H S V I S D S P R S W I Q V Q I P A S H P V L
981  AGCAACAATGCCCTCACAGGTCATATCTGACAGCCCGAGATCCTGGATACAGGTGCAGATCCCTGCATCTCATCTGTCC
    T L S P E K A L N F E G T K V T L H C E T Q E D S L
961  TCACTCTCAGCCCTGAAAGGCTCTGAATTTTGAAGGAACCAAGGTGACACTTCACTGTGAACCCAGGAAGATTCTCTG
    R T L Y R F Y H E G V P L R H K S V R C E R G A S I S
1041  CGCACTTTGTACAGGTTTATCATGAGGGTGTCCCTGAGGCACAAAGTCAGTCGCTGTGAAGGGAGCATCCATCAG
    F S L T T E N S G N Y Y C T A D N G L G A K P S K A V
1121  CTTCTCACTGACTACAGAGAATTCAGGGAATCTACTGACAGCTGACAATGGCTTGGCCCAAGCCAGTAAGGCTG
    S L S V T V P V S H P V L N L S S P E D L I F E G A
1201  TGAGCCTCTCAGTCACTGTTCCCGTGTCTCATCTCTCACTCAGCTCTCTGAGGACCTGATTTTGTAGGGAGGCC
    K V T L H C E A Q R G S L P I L Y Q F H H E D A A L E
1281  AAGGTGACACTTCACTGTGAAGCCCAAGAGAGGTTCACCTCCCATCTCTGTACCAGTTTCATCATGAGGATGCTGCCCTGGA
    R R S A N S A G G V A I S F S L T A E H S G N Y Y C T
449

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FIGURE 6c-1A

1361	GGTAGTGGCCCAACTCTGCAGGAGGAGTGGCCATCAGCTTCTCTGACTGCAGAGCAATTTCAGGGAACTACTGTGCA	475
1441	A D N G F G P Q R S K A V S L S I T V P V S H P V L	
1521	CAGCTGACAAATGGCTTTGGCCCCCAGCGCAGTAAGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCTGTCCCTC	502
1601	T L S S A E A L T F E G A T V T L H C E V Q R G S P Q	
1681	ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCACTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCCCCACA	529
1761	I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F	
1841	AATCCTATACCAGTTTATCATGAGGACATGCCCTCTGTGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTTCAGCT	555
1921	S L T E G H S G N Y Y C T A D N G F G P Q R S E V V	
2001	TCTCTGACTGAAGGACATTCAGGGAATTACTACTGCACAGCTGACAAATGGCTTTGGTCCCGCAGCGCAGTGAAGTGGTG	582
2081	S L F V T V P V S R P I L T L R V P R A Q A V V G D L	
2161	AGCCTTTTGTCACTGTTCCAGTGTCTCGCCCCATCTCTCACCCCTCAGGGTTCAGGGCCCGCAGGCTGTGGTGGGGACCT	609
2241	L E L H C E A P R G S P P I L Y W F Y H E D V T L G S	
2321	GCTGGAGCTTCACTGTGAGGCCCGAGAGGCTCTCCCCCAATCCTGTACTGGTTTATCATGAGGATGTACCCCTGGGGA	635
2401	S S A P S G G E A S F N L S L T A E H S G N Y S C E	
2481	GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTTCAACCTCTCTCTGACTGCAGAACTTCTGGAACCTACTCATGTGAG	662
2561	A N N G L V A Q H S D T I S L S V I V P Y S R P I L T	
2641	GCCAAACAATGGCCTAGTGGCCCCAGCACAGTGACACAAATATCACTCAGTGTATAGTTCAGTATCTCGTCCCATCTCAC	689
	F R A P R A Q A V V G D L L E L H C E A L R G S S P I	
	CTTCAGGGCTCCAGGCCAGGCTGTGGTGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCAA	715
	L Y W F Y H E D V T L G K I S A P S G G G A S F N L	
	TCCTGTACTGGTTTATCATGAAGATGTACCCCTGGTAAAGATCTCAGCCCTCTGGAGGAGGGCCCTCTTCAACCTC	742
	S L T T E H S G I Y S C E A D N G L E A Q R S E M V T	
	TCTCTGACTACAGAACATTTCTGGAATCTACTCTCTGTGAGGCAGACAATGGTCTGGAGGCCCGCAGCGCAGTGAATGGTGAC	769
	L K V A V P V S R P V L T L R A P G T H A A V G D L L	
	ACTGAAAGTTGCAGTTCGGTGTCTCGCCCGGTCTCTCACCCCTCAGGGCTCCCGGACCCATGTGCGTGGGGACCTGC	795
	E L H C E A L R G S P L I L Y R F F H E D V T L G N	
	TGGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCCCCTGATCCTGTACCGGTTTTCATGAGGATGTACCCCTAGGAAT	822
	R S S P S G G A S L N L S L T A E H S G N Y S C E A D	
	AGTCTGTCCTCTGAGGAGCGTCTTAAACCTCTCTGACTGCAGAGCACCTCTGGAACCTACTCTCTGTGAGGCCGA	849
	N G L G A Q R S E T V T L Y I T G L T A N R S G P F A	
	CAATGGCCTCGGGGCCCGCAGTGAGACAGTGTATATCATCAGGGCTGACCCCGAACAAGTGGCCCTTTTG	875
	T G V A G G L L S I A G L A A G A L L Y C W I S R	
	CCACAGGAGTGGCGGGCCCTCTCAGCATAGCAGGCCCTGTCTGGGGGCACTGTCTCTACTGTCTGTCTCTCGAGA	902
	K A G R K P A S D P A R S P S D S Q E P T Y H N V	

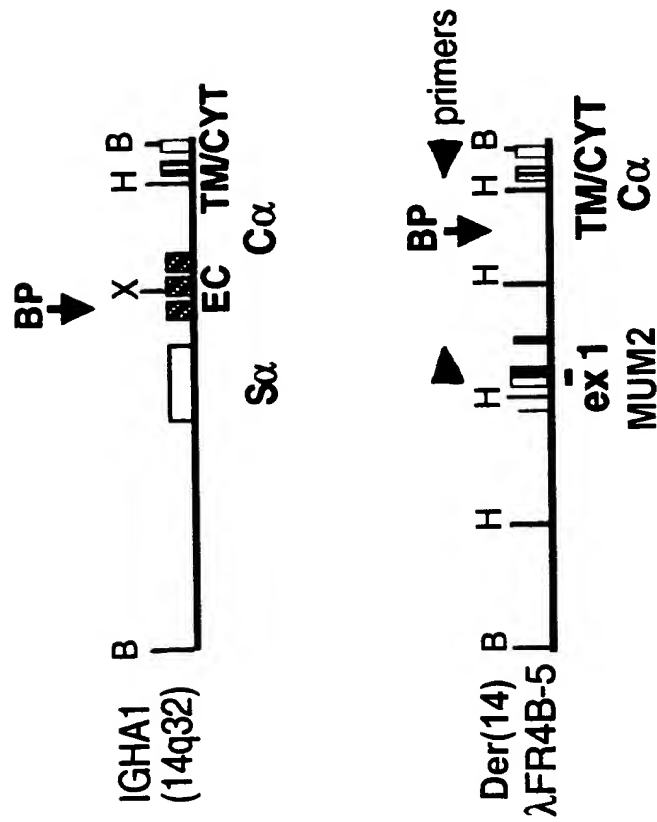
FIGURE 6c-1B

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2721 AAAGCAGGGAGAAAGCCCTGCCTCTGACCCCGCCAGGAGCCCTTCAGACTCGGACTCCCAAGAGCCCCACCTATCACAATGT
    P A W E E L Q P V Y T N A N P R G E N V V Y S E Y R I 929
2801 ACCAGCCTGGGAAGAGCTGCCAACCCAGTGTAACACTAATGCCAAATCCTAGAGGAGAGAAATGTGGTTTACTCAGAAAGTACGGA
    I Q E K K K H A V A S D P R H L R N K G S P I I X S 955
2881 TCATCCAAGAGAGAAAGAAACATGCAGTGGCCTCTGACCCCGAGGCATCTCAGGAACAAGGGTTCCCTTATCATCTACTCT
```

	E	V	K	V	A	S	T	P	V	S	G	S	L	F	L	A	S	S	A	P	H	R	.	stop	
2961	G	A	A	G	T	T	A	A	G	G	T	T	C	C	G	A	T	C	C	T	G	T	T	C	C
3041	T	C	T	C	A	A	C	T	G	T	T	C	C	G	A	T	C	C	T	G	T	T	C	C	T
3121	G	C	C	C	A	G	C	C	T	G	C	A	C	C	C	A	A	G	T	T	C	C	C	T	T
3201	T	C	A	C	T	G	T	T	C	C	A	T	A	C	T	G	T	T	C	C	A	T	T	C	C
3281	A	T	C	T	C	T	G	A	T	T	C	T	G	G	C	T	G	T	T	C	C	A	T	T	C
3361	T	T	A	C	C	A	C	A	A	G	G	A	G	A	G	T	G	G	C	T	T	C	C	A	A
3441	A	G	T	T	C	T	G	T	T	C	C	A	T	T	C	T	C	A	A	T	T	G	T	C	A
3521	C	A	C	A	G	C	T	G	C	A	T	G	G	A	C	A	T	G	T	G	G	T	C	T	C
3601	C	T	A	A	G	G	T	C	C	C	A	C	G	G	G	T	G	C	A	T	T	C	T	C	T
3681	T	A	C	A	C	A	G	T	C	C	C	A	A	G	T	A	C	C	A	A	G	T	A	C	C
3761	G	A	A	C	A	C	A	T	G	G	A	G	T	G	T	C	A	A	T	T	A	C	T	T	A
3841	T	G	T	G	G	T	A	T	C	A	A	T	C	C	A	T	T	A	C	T	T	A	C	T	T
3921	G	A	A	G	A	G	A	G	T	T	C	C	A	A	G	A	A	T	C	C	C	T	T	C	T
4001	G	A	G	A	T	C	T	G	A	T	A	C	A	T	A	C	A	T	T	A	C	T	T	A	C
4081	A	T	G	T	G	T	G	T	G	G	C	T	G	G	A	C	T	G	C	A	T	G	T	G	T
4161	A	T	G	T	G	G	T	C	T	G	G	C	T	G	G	A	C	T	G	C	A	T	G	T	G
4241	C	A	C	A	G	T	G	T	G	T	G	C	T	G	A	G	A	G	T	T	C	T	G	A	G
4321	T	G	C	A	C	T	A	T	C	T	T	T	C	C	C	A	C	T	G	A	G	A	G	A	G
4401	A	T	T	C	A	G	A	T	T	C	C	A	T	C	T	G	A	G	A	T	G	T	A	T	A
4481	T	T	T	G	T	C	C	C	A	G	T	G	T	T	C	T	G	T	T	C	C	G	T	T	C
4561	T	C	A	C	T	C	C	A	G	T	G	A	T	G	A	T	C	C	A	T	C	C	A	T	C
4641	C	A	A	C	T	T	C	A	A	G	G	A	A	C	C	A	A	G	T	T	C	A	A	G	A
4721	G	A	G	G	C	T	T	T	C	A	T	G	T	T	C	A	A	G	T	T	C	A	A	G	A
4801	T	T	A	G	C	T	A	G	T	T	G	A	A	G	T	T	C	A	A	G	T	T	C	A	A
4881	C	T	G	A	G	G	T	C	A	T	C	A	A	G	T	C	A	A	G	T	T	C	A	A	G
4961	T	A	G	A	T	T	C	A	T	G	G	A	G	A	T	A	G	T	T	C	A	A	G	A	A
5041	G	T	G	G	T	G	A	C	C	C	A	T	C	C	C	A	T	C	C	A	T	C	C	A	A
5121	G	C	T	T	G	G	C	T	G	A	C	A	T	A	G	G	C	T	T	A	T	T	C	C	T
5201	A	T	A	T																					

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FIG. 7A



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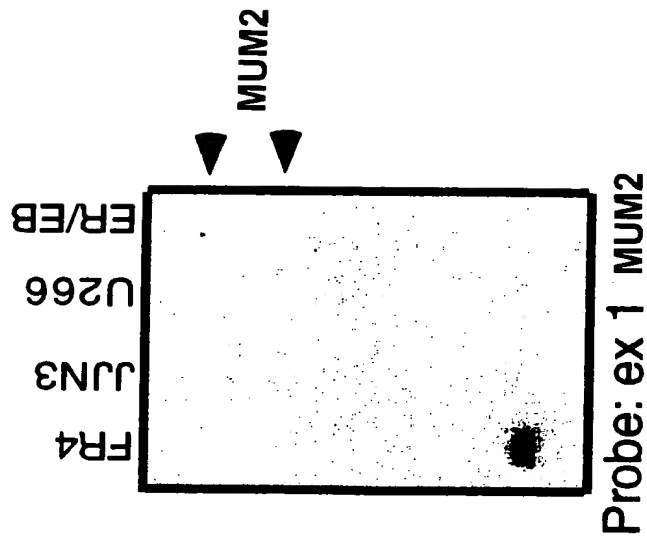


FIG. 7B

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FIG. 7C

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1  CTCAATCAGCTTTATGTCAGAGAGAAGCTTACTGAGCTCACTGCTGGTGGTGTAGGCAAGTGC'TGCTTTGGCAA
78  TCTGGGCTGACCTGGCTTGTCTCAGAACTCCTTCTTCCAAACCTGGAGCAGGCTTCCATGCTGCTGGGCGTCC
   L L A F A P V C G Q S G S C S V A D W Q M P P P Y V
155 TTGCTGGCCTTTGCTCCAGTCTGTGGACAATCTGGCTCTTGTCTGTTCAGATTGGCAGATGCCGCTCCCTATGT
   V L D L P Q E T L E E T P G A N L W P T T L T F L
232 GGTGCTGGACTTGCCGCGAGGAGACCTGGAGGAGAGACCCCGCGCCCAACCTGTGGCCCCACCACCATCACCTTCC
   T L F L L S L F Y S T A L T V T S V R G P S G N R
309 TCACCCCTCTTCCTGCTGAGCCTGTTCTATAGCACAGCACTGACCCGTGACCCAGCGTCCGGGGGCCCATCTGGCAACAGG
   E G P Q Y .
386 GAGGGCCCCCAGTACTGAGCGGGAGCCGGCAAGGCACAGTGGGAGCCCAAGAGGGGATGAGCCACAGTGGATGA
463 GGTGGGCTGCAGTGTGGCTAAGAGGAGAGCACCACTGTCTCCCACTGTGGGGGACGTGCTCTCTGGGGGGCCC
540 TTCACAGACACTGAGGACACGCGAGGCCCAAGGTCAGGGCTGAGCTTCCCTCCAGTGCAGTAACGAGGATTCCGTC
617 CAGGCTCCCATGAGCAGGCCAGGGCTGAGACAGAGGGCGTTGGCAAGGATGCTGCTTTCAGGCTGTGACCCCTCTG
694 TCTTTCAGGGAGGAAAGTGTGAGGAACCTCTTGGAGAAGCCAGCTATGCTTGGCCAGAACTCAGCCCTTTCAGACGT
771 CACCGACCCGCCCTTACTCACAATGCTTCCAGGTGCAATAAGTGGCCCCCAAGGAAAAA

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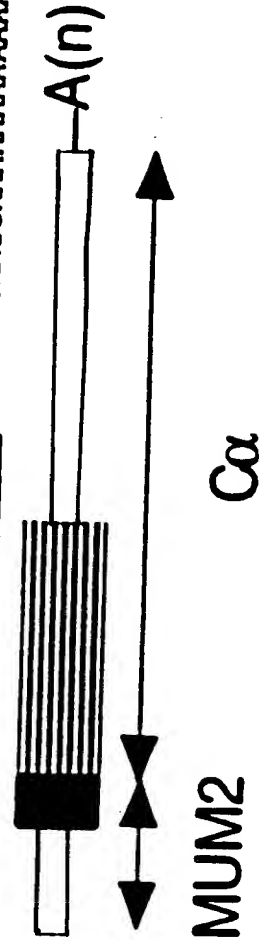


FIGURE 8A

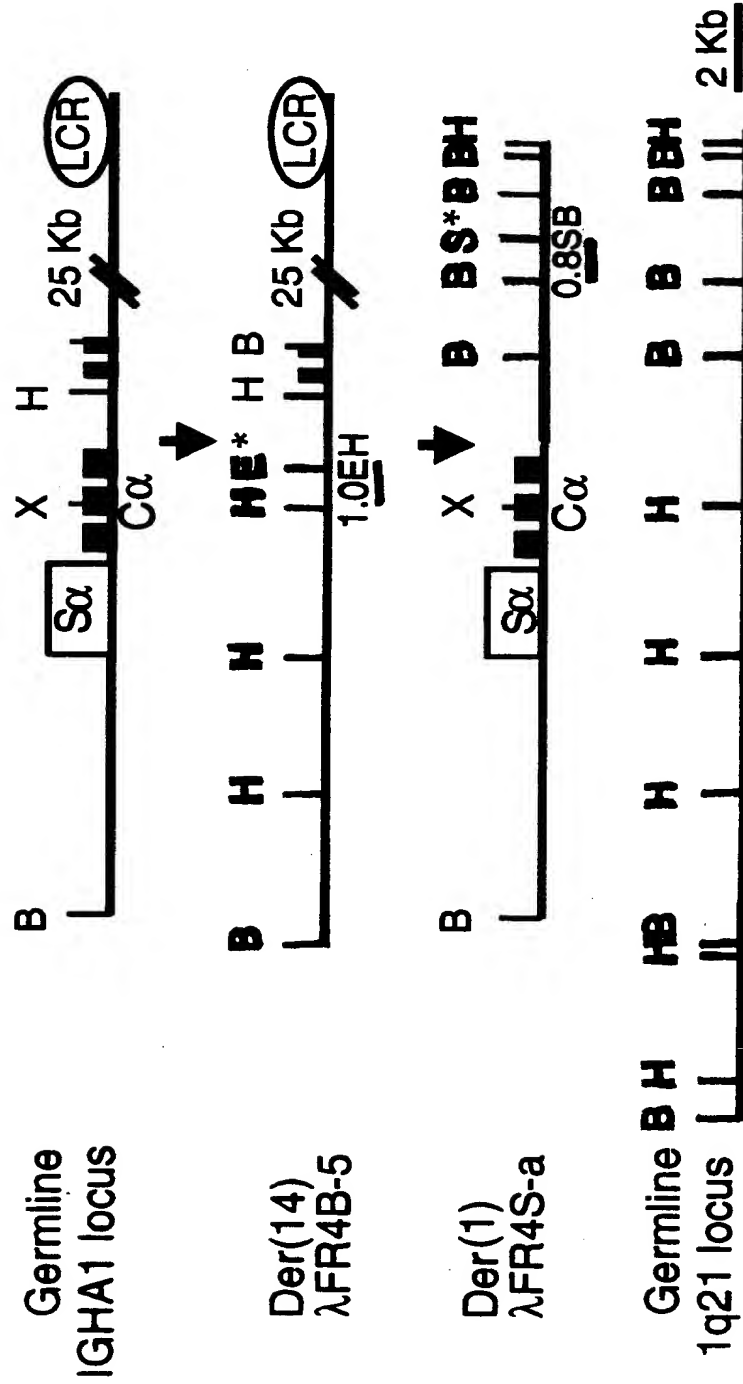
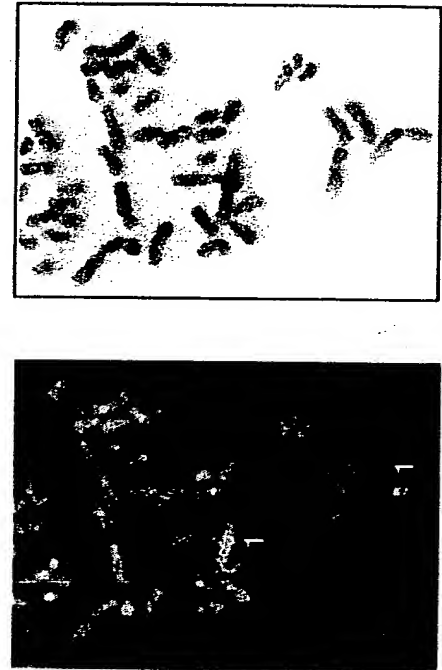


FIG. 8B

Chr 14 TCCCACTGACGCATGCAGGAAGGGCACCTCCCTTAAACACACTGCTCTGTACGGGGGACGTTGGGCACAGGTGCACACTCACA
 Der (14) GGCCTGACAGCAACTTTTCTTCTACTAGTTCATCTTAA- CACACTGCTCTGTACGGGGGACGTTGGGCACAGGTGCACACTCACA
 Chr 1 GGCCTGACAGCAACTTTTCTTCTACTAGTTCATCTTAACTTATCCTGTTAACTGGCGAGACAACTGTCTTAACTGAAGGGAAA
 Chr 1 GGCCTGACAGCAACTTTTCTTCTACTAGTTCATCTTAACTTATCCTGTTAACTGGCGAGACAACTGTCTTAACTGAAGGGAAA
 Der (1) TCCCACTGACGCA ----GGAAGGATCTTAAAGTTTATCCTGTTAACTGGCGAGACAACTGTCTTAACTGAAGGGAAA
 Chr 14 TCCCACTGACGCA TGCAGGAAGGGGCACCTCCCTTAACTGACACACTGCTCTGTACGGGGGACGTTGGGCACAGGTGCACACTCACA

FIG. 8C



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FIG. 9A

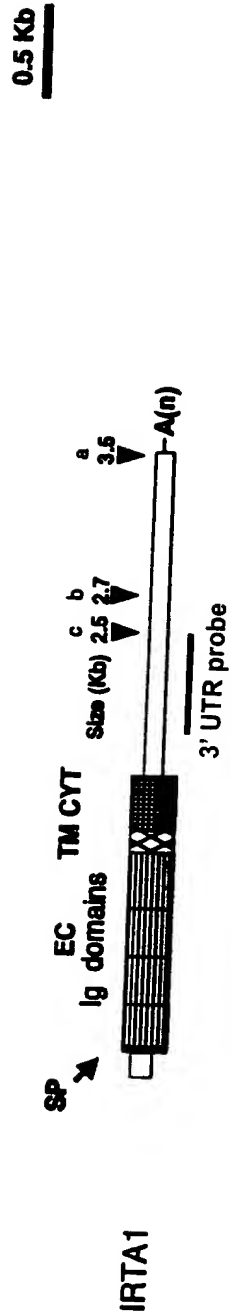
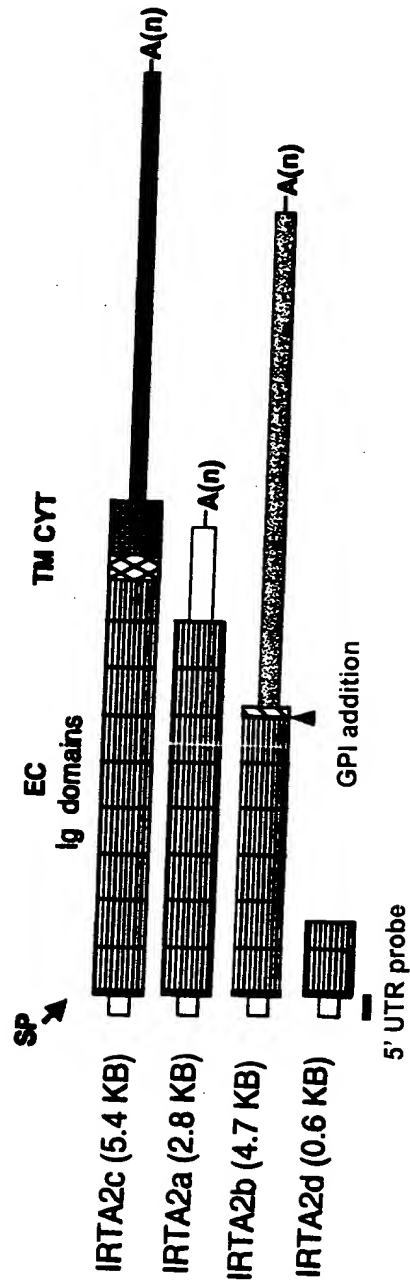


FIG. 9B



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FIGURE 10A

FCGR1IA	(1)	MAMETQMSQNVCPRNLLWLLQPPVAVLLASADSSAAAPKAVLKLEPPVAVLVLEDSVLTTCQCARSPEDSLOPHNGNIPTHIQPSYRFRKANNNDSC
FCGR1IA	(1)	-----MWQLPPPAHLLVSAGMRTEDLPAHVVFLPQYRMLKDSVTLKQCAYSPEDNSTQWFHNESSISQAASSYFIADAVVYDSC
FCERIA	(1)	-----MAP-AMESPTLCVADLEFPADCVLAVPQPKVSLNPPNRIKGENVLTQGNNEFEVSTKPHNGSSEETNSSLNINVKFEDSC
FCGR1A	(1)	-----MWFLTTLVLLWVPDGVV-DTIRAVTSLQPPVSVFQBEVTLHCEVLHILFGSSSTQWELNGTATQTSIPSYRITSSVANDSC
IRTA-1	(1)	-----MLTWASLTLAFAPVCEQSAAHKRPVLSVHPPTTFEKGERRVLTQNCQFQYATEKTLVYERHYWGEKLLILTPGNT-LEVRRESC
IRTA-2	(1)	-----MLTWVTLVVLAPVSGCFARTERPILFLQPPWTIVFQGERVLTQKCFRFYSPQKTKVYRYLKGKELLRETTPDNI-LEVQESG
FCGR1IA	(101)	EVTCCQTGQTSLSDPVHETVLSFWLVLTQTEHLEFCQGETIMLRCHSMKDKPVMKVTFFQNGKSKESRLDPTESIPQFNHSHSDMHCICNICVTL-FSSK
FCGR1IA	(86)	EXRCQTNLSLTSDPVQLEVHIGWLLLOAFRWVEKEDEIHLRCHSMKNTADHNTVTLQNGSGRKYFHHNSDEYIPKETLKESSMFRGLFESKN-VSSK
FCERIA	(90)	EYKCCHQVNESEPVYLEVFSDWLLLOQASAEVVMGCEPLFRCHGGRNWDVAKVIVYKDCGELIYWYEHNISITNAIVELSETVYCTGKVMQLD-YESE
FCGR1A	(82)	EYRCGRGLSGRSDFIQLEIHRGWLLLOQVSSRVFTEGEPALARCHAMRDKLVVNLVYRNGKAFKEFFHWSNLTLTKTNI SHNGTYHSG-NCKHR-YTSA
IRTA-1	(82)	LVRQCARGPSRNPVRILFSSDSLLOAFYSVF-EGDILVLRCHRRRKEKLTAKKVTWNGNIIISINKSWGLLIPQASSNNNENRGLIYGDENDVFRSN
IRTA-2	(82)	EYRCQAQGSPTSSPVLHIDFSSASLLOAFLSVF-EGLSVLRGRAKAEVTLANNYIK-NDNVTLNKRTRDEHHPHACLKQNGAIRCIGYKESCCPVSSN
FCGR1	(172)	CKHR--YTSAGISVTVKELFFAPVLNASVTSLELEGNLVTLSCETKILLQRPGLQLVESEFYMGSLTL-PRNTSSEYQILLTPRRDSGLTWCEAATIEDGN
IRTA-1	(171)	EDENDVFRSNFKITKIQELFFHEELKATDSQI-TEGNSVNLSCETQPPERSDTPLHNEFFRDGEVLSDWSTYPEILPLPVWRENSGSLTWCEATVVRGN
IRTA-2	(170)	KECCCPVSSNTVYKIQOEFETRPVTRPVRASSFOI-ISENPVTLICETQUSIERSDVPLRERFERIDQILGLQASLSSENFOTIAMS KDSGFWGKATMPHS
FCGR1	(269)	VLRSPPELEQLGLQLPTPVWFHVLGYLAUGIMEFLVNVLVWVIRKEEXRKKKKWDLEISLDSGHEKVTSSLOEDRHLLEELKQCE-OKEEQLOQEQVHR
IRTA-1	(270)	IHKHSPSTQTHVGRIPVSGVL-LETOISGGQAVEGEMLVVCVAEGTGDITFSWHRQDMQESLGNKQTSRLRAELETPAIRQSHAE-CXYCTADNSYC-
IRTA-2	(269)	VISDSPRSWIOVG-IRASHPV-LTISPEKALNFECKVTLHCEQOEDSIRTDYRFYHEGV--PIRHKSVRCERGASISFSLITENSE-NVYCTADNGLCA

FIGURE 10B

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E      E      I      I
DTM:  DXXXXXX--DXX--YXXLXXXXXXXX--YXXL

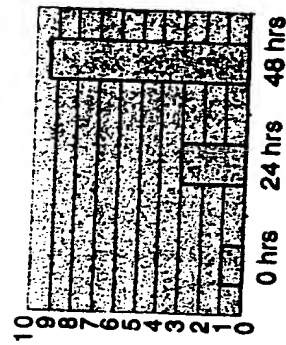
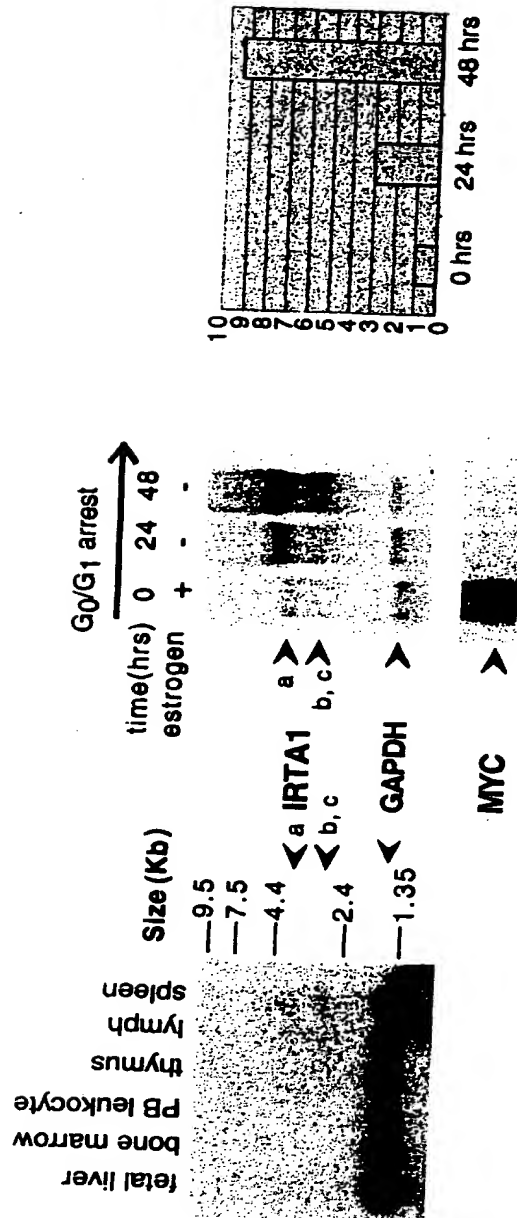
IRTA-1:  ESSHSICPAQVELQSLYVDVHPKKG-DLVYSEIQTTTLGEEEEEAANTSRTLLEDKDVSVVYSEV
PECAM:    DNKEPLNSDVQYTEVQVSSAEWSHK-----DLGKKDTEVTYSEV
IRTA-2C:  DSDSQ---EPTYHNVPAAWEELQPVYT-----NANPRGENVVYSEV
BGP-1:    ASDQR---DLTEHKPSVSNHTQDHSN-----DPPNKMNEVTYSTL

ITIM:     SXYXXL      SXYXXL      SXYXXL
          V      V      V
          L      L      L
          I      I      I

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FIGURE 11A

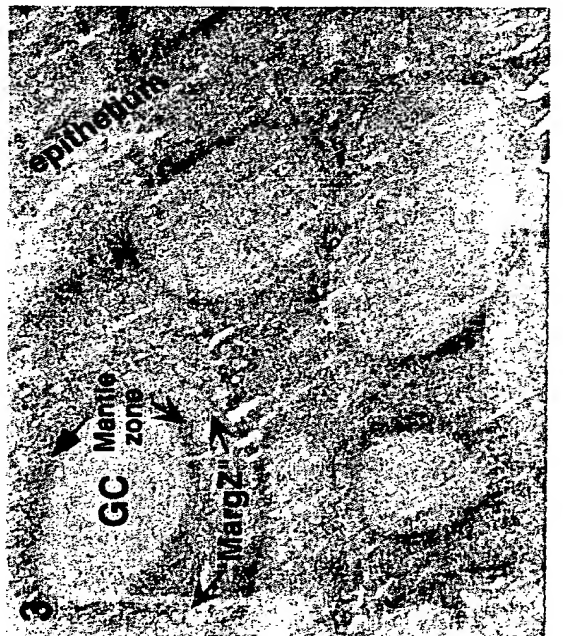
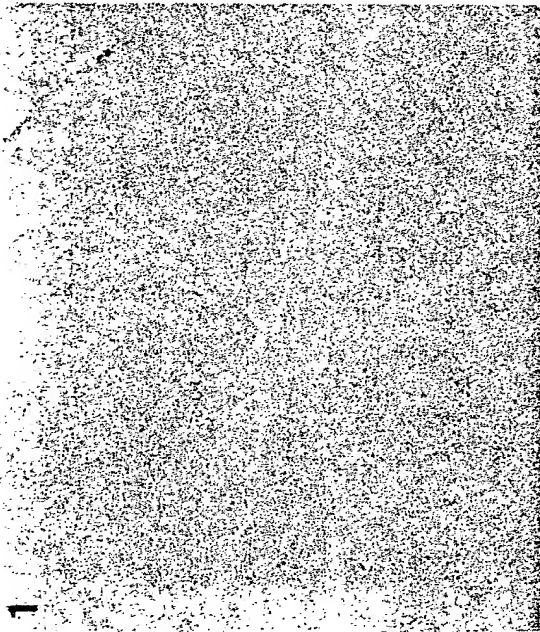


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FIGURE 11B1-B4

11B1-4



Size (Kb)

9.5

7.5

4.4

2.4

1.35

GAPDH

c

b

a

d

PB leukocyte

lung

placenta

small intestine

liver

kidney

spleen

thymus

colon

skeletal muscle

heart

brain

fetal liver

bone marrow

PB leukocyte

thymus

lymph

spleen

RD

NC42

CB33

EREB

FR4

MOL T4

HUT78

HL60

K562

U937

MM T cell

Myel Ery Mono

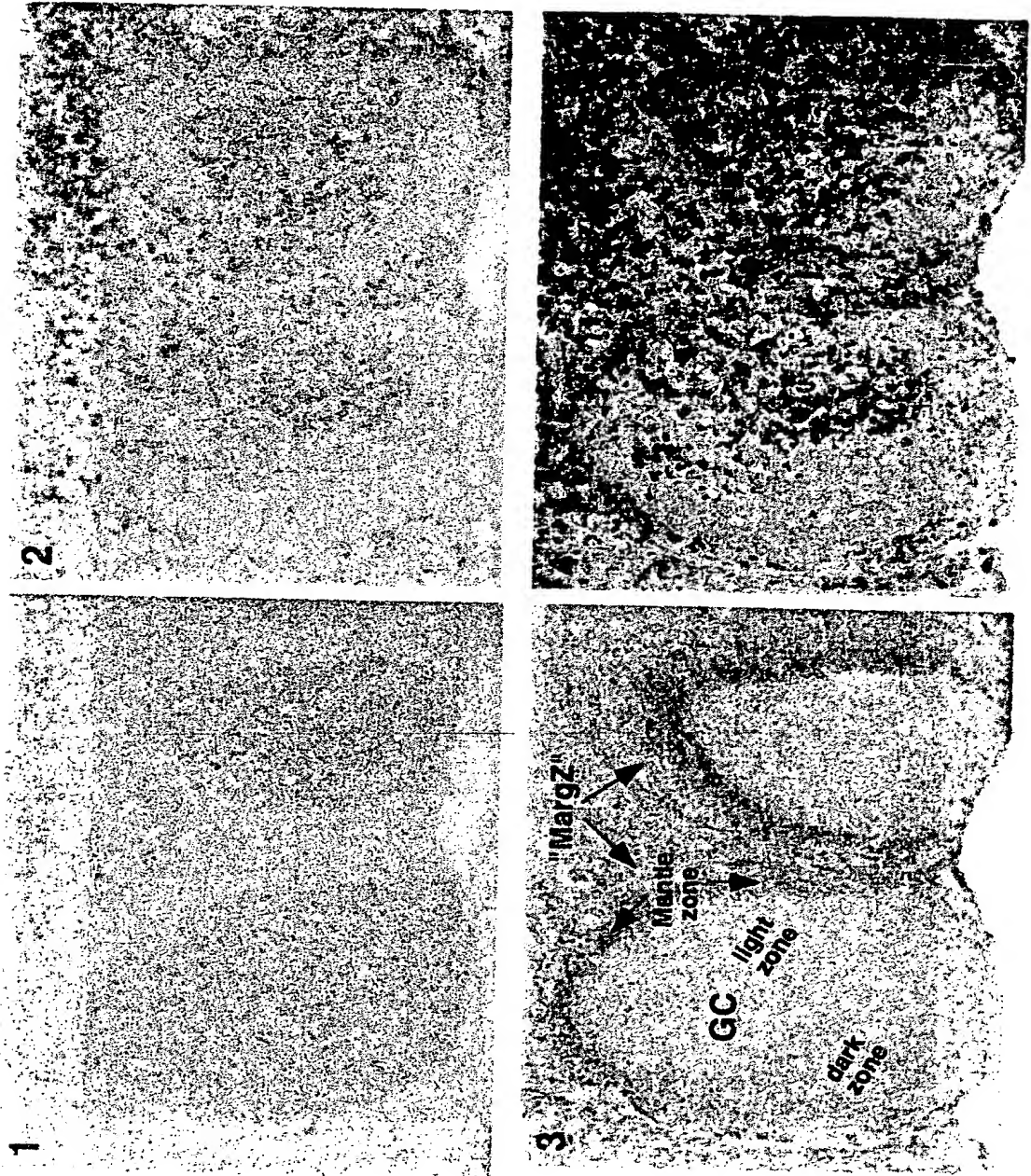
LCL

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FIGURE 12B1-B4

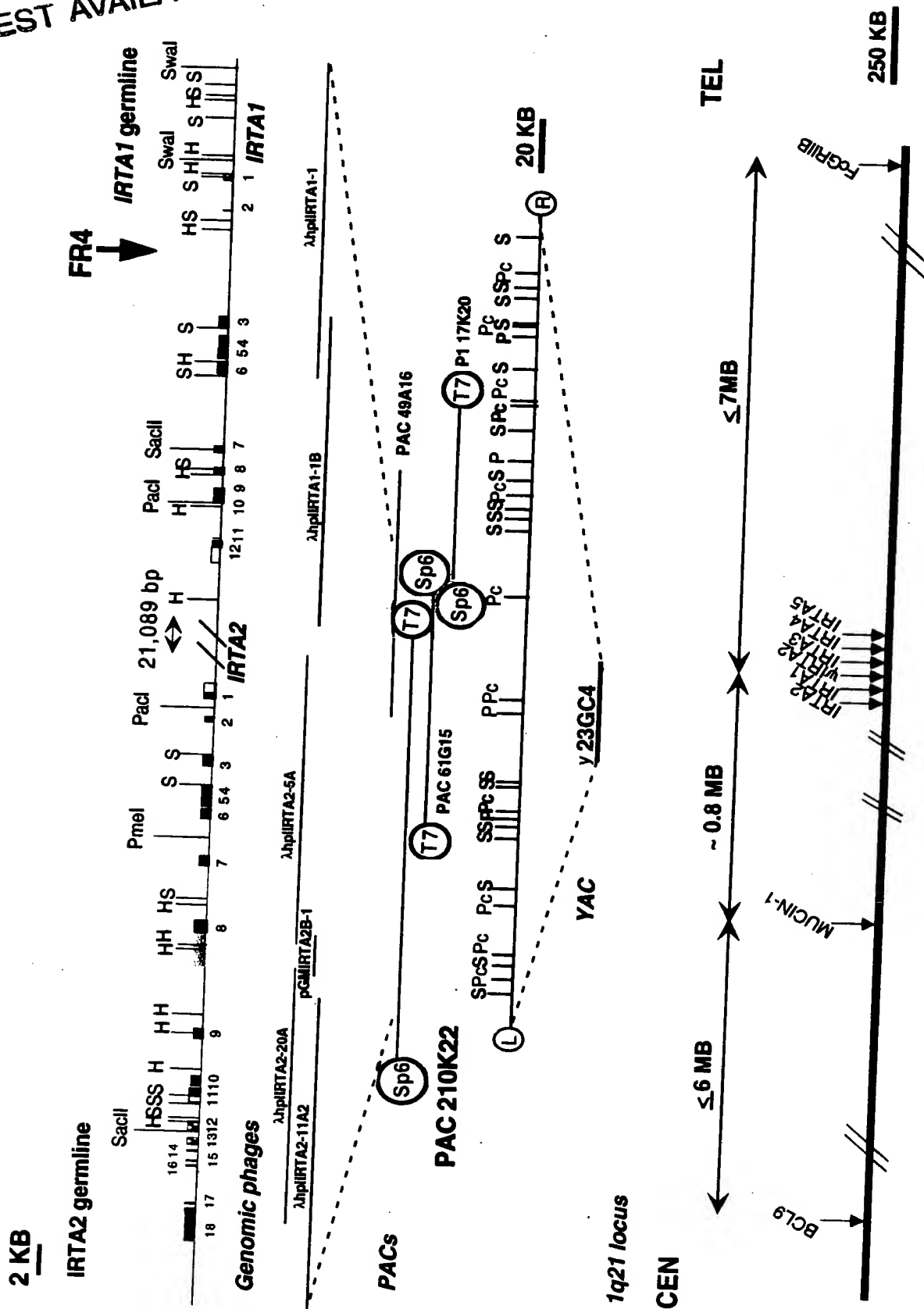
B



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FIGURE 13



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FIG. 14B

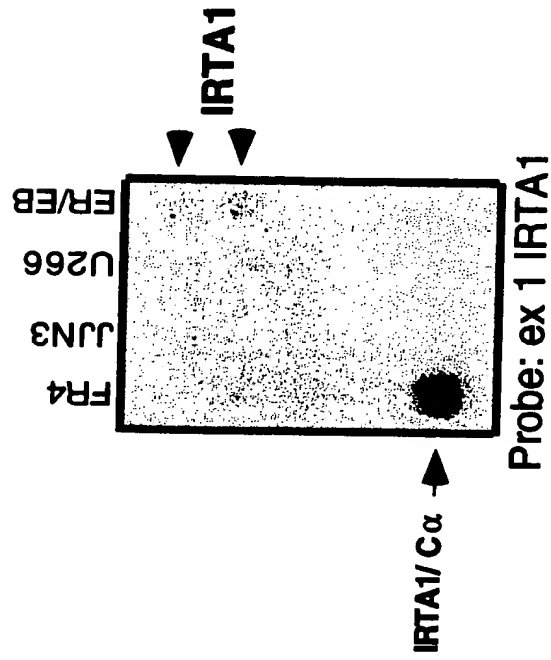


FIG. 14A



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FIG. 14D

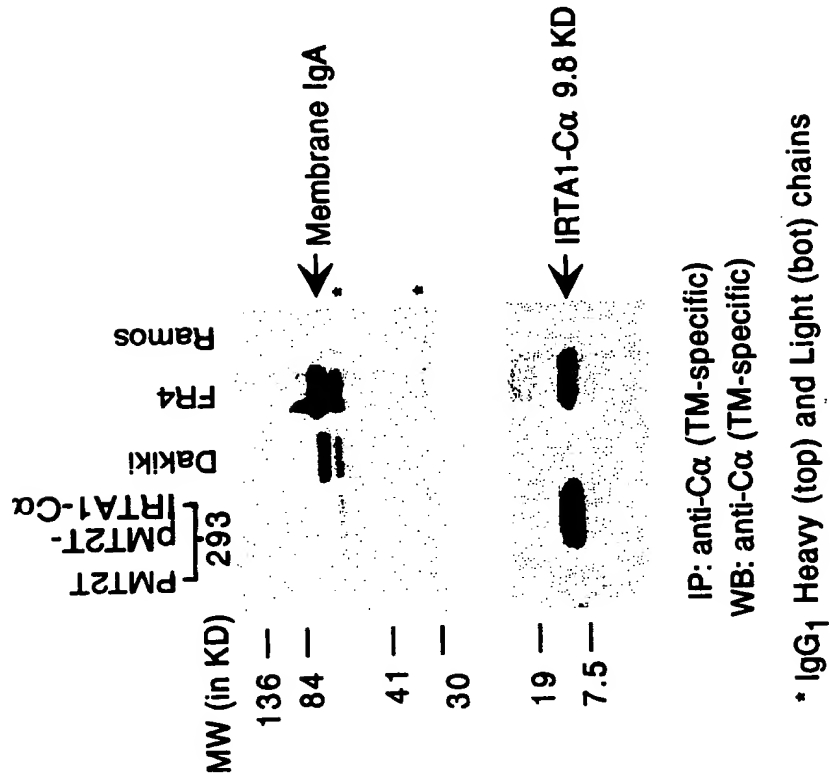


FIG. 14C

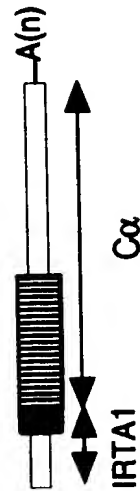


FIG. 15A

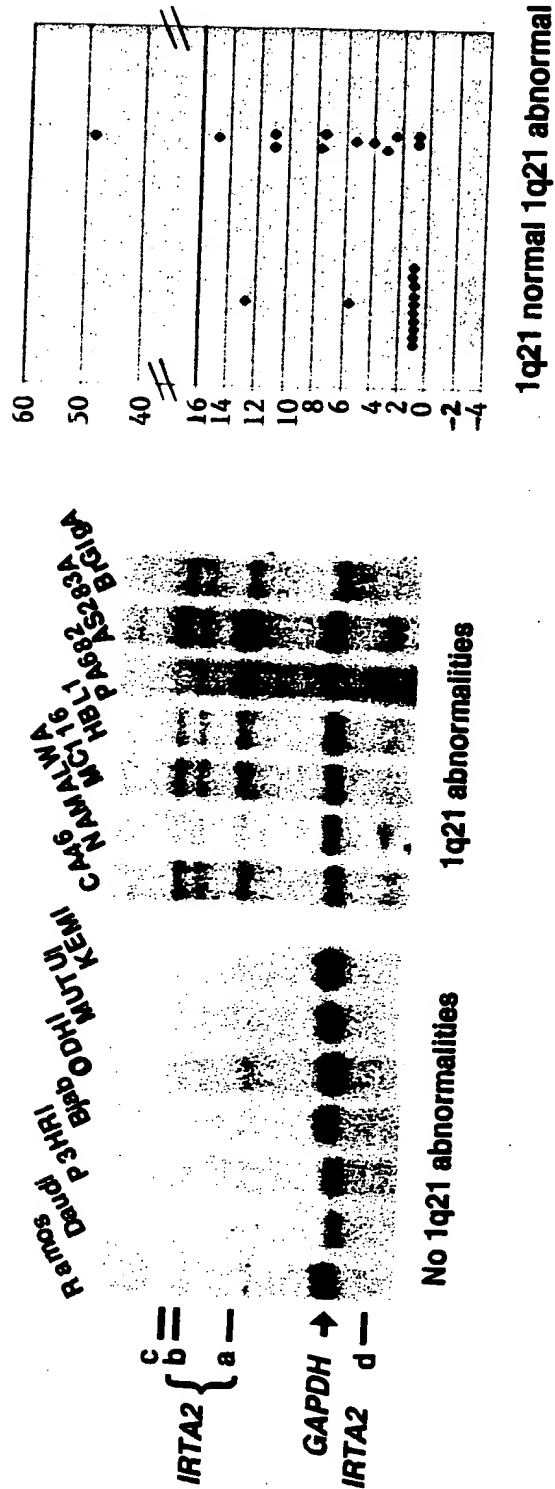
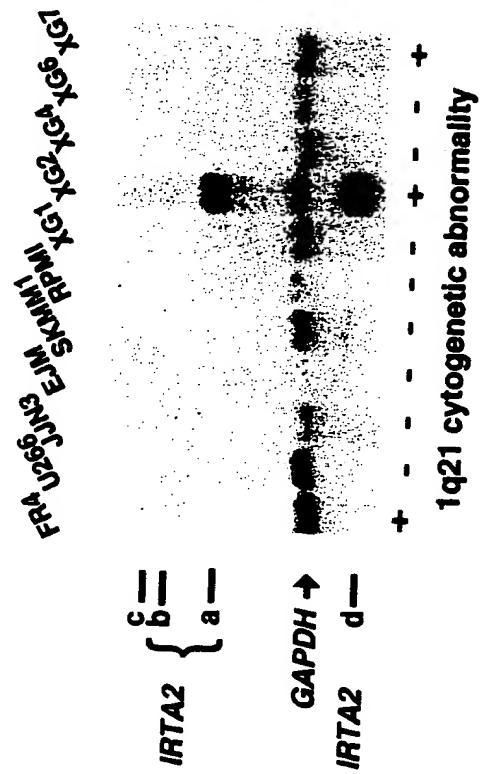


FIG. 15B

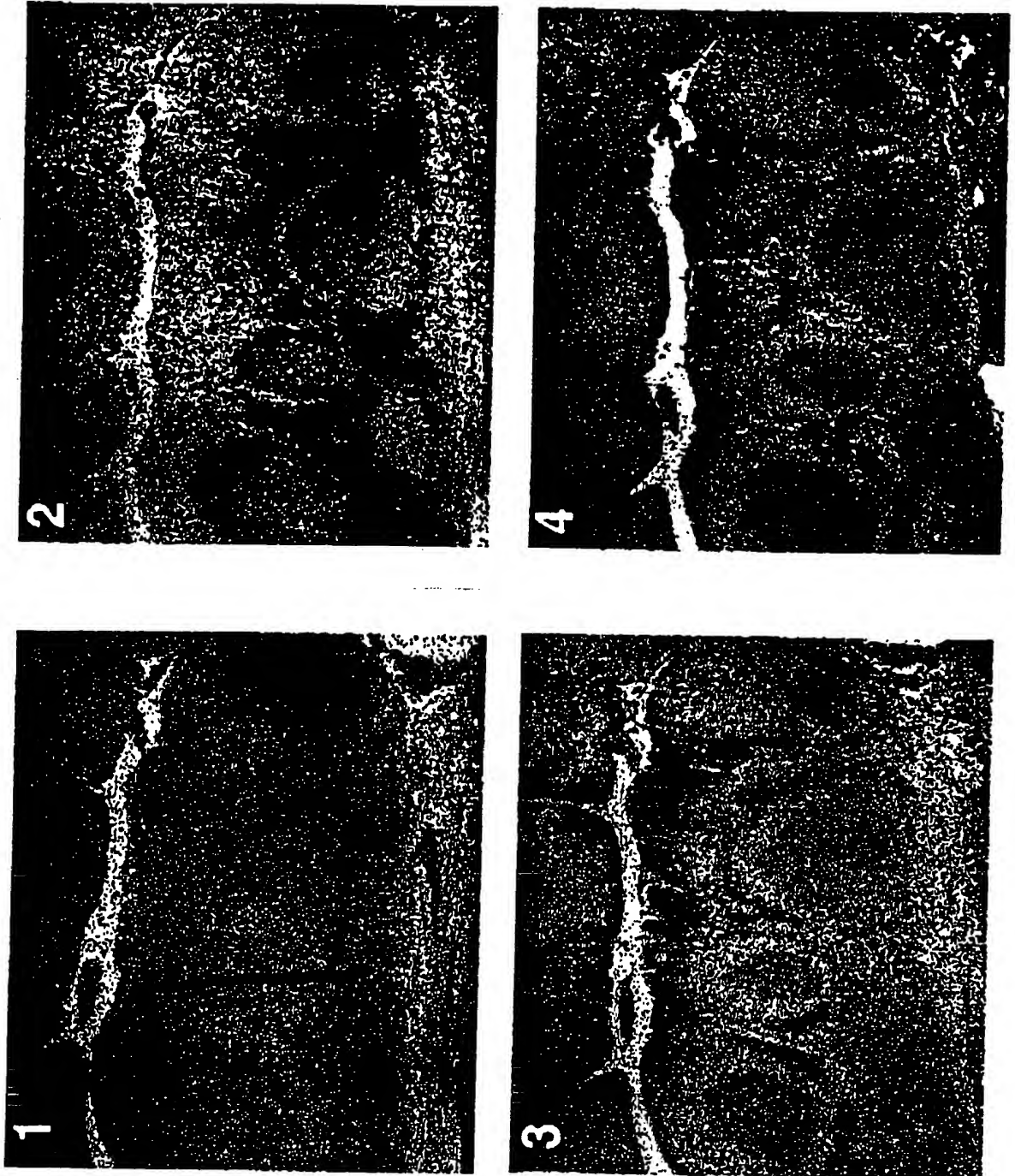


Cell line	IRTA2
Burkitt Lymphoma	
Normal 1q21	2/12
Abnormal 1q21	10/12
Multiple Myeloma	
Normal 1q21	0/7
Abnormal 1q21	1/3

Summary of IRTA2 expression

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FIGURE 16-1-1~16-4
IRTA1 expression in normal lymphoid tissue

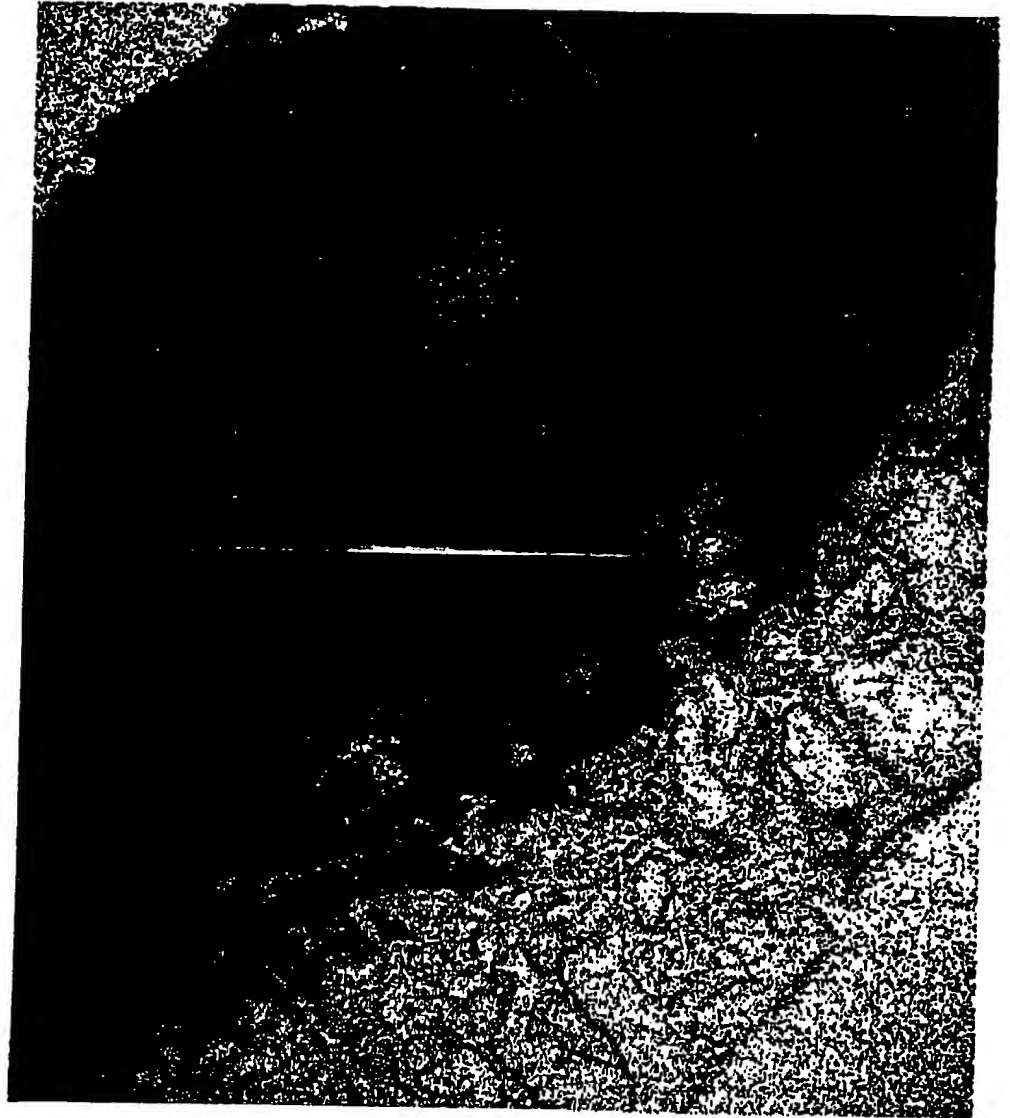


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FIGURE 17

IRTA1 expression in a stomach Mucosa-Associated-Lymphoid Tissue B cell lymphoma



1 CTCAATCAGCTTATGCAGAGAAAGCTTACTGAGCTCACTGCTGGTGTGGTGTGGCAAGTCTGCTTTGGCAA M L L W A S

78 TCTGGGCTGACCTGGCTTGTCTCTCAAACTCCTTCTCCAACCCCTGGAGCAGGCTTCCATGCTGCTGTGGCGTCC L L A F A P V C G G S A A A H K P V I S V H P P W T

155 TTGCTGGCCTTGTCTCCAGTCTGTGGACAATCTGAGCTGCACACAAACCTGTGATTCCTCGTCCATCCTCCATGGAC T F F K G E R V T L T C N G F Q F Y A T E K T T W Y

232 CACATTCTTCAAGGAGAGAGTGTGACTCTGACTTGCATGCAATGGAATTCAGTTCTATGCAACAGAGAAACAACATGGT H R H Y W G E K L T L T P G N T L E V R E S G L Y

309 ATCATCGGCACTACTGGGGAGAAAGTTGACCTGACCCCGAGGAACACCCCTGAGGTTCTGGGAATCTGGACTGTAC R C Q A R G S P P S N P V R L L F S S D S I L Q A

386 AGATGCCAGGCCGGGGCTCCCCACGAAGTAACCCCTGTGCGCTCTCTTTTTCITCAGACTCCTTAATCTGCAGGC P Y S V F E G D T L V L R C H R R R K E K L T A V K

463 ACCATATCTGTGTTGAGGTCGACATCTGGTCTGAGATGCCACAGAAGAGGAAGAAATTTGACTGCTGTGA Y T W N G N T L S I S N K S W D L L I P Q A S S N

540 AATATACTTGGAAATGGAACATCTCTTCCATTTCTAATAAAAGCTGGGATCTTCTATCCCAAGCAAGTTCAAAT N N G N Y R C I G Y G D E N D V F R S N F K I I K I

617 AACAAATGGCAATATCGATGCAATGGATATGGAGATGAGAATGATGATTTAGATCAAAATTTCAAATATATTAAT Q E L F P H P E L K A T D S Q P T E G N S V

694 TCAAGAACTATTTCACATCCAGAGCTGAAAGCTACAGACTCTCAGCCTACAGAGGGGAATTCGTAAACCTGAGCT E T Q L P P E R S D T P L H F N F R D G E V I L

771 GTGAACACACAGCTTCTCCAGAGCGGTGAGACACCCCACTTCACTCAACTTCTTCCAGAGATGGCGAGTCACTCTG S D W S T Y P E L Q L P T V W R E N S G S Y W C G A

848 TCAGACTGGAGCAGTACCCGGAATCCAGCTCCCAACCGTCTGGAGAGAAAACCTCAGGATCCTATTGGTGTGGTGC E T V R G N I H K H S P S L Q I H V Q R I P V S G V

925 TGAACACAGTGAGGGTAACATCCACAGCACAGTCCCTCGTACAGATCCATGTGAGGCGGATCCCTGTGTCTGGG L L E T Q P S C G G Q A V E G E M L V L V C S V A E

1002 TGCTCCTGGAGACCCGCCCTCAGGGGGCCAGGCTGTGAAGGGGAGATGCTGGTCTCTGTCTCCTCCGTGGGTGAA G T G D T T F S W H R E D M Q E S L G R K T Q R S L

11079 GGCACAGGGGATACCAATTTCTCTGGCACCGGAGGACATGCAGAGAGTCTGGGAGGAAAACCTCAGCGTCCCT R A E L E L P A I R Q S H A G G Y Y C T A D N S Y G

1156 GAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGAGCCATGCAGGGGATACTACTGTACAGCAGACACAGCTACG P V Q S M V L V T V R E T P G N R D G L V A A G

1233 GCCCTGTCCAGAGCATGGTGTGAATGTCACTGTGAGAGAGACCCAGGCAACAGAGATGGCCTTGTGCGCGCGGA A T G G L L S A L L L A V A L L F H C W R R R K S G

1310 GCCACTGGAGGGTGTCTCAGTGTCTTCTCCTGGCTGTGGCCCTGTGTTTCACTGCTGGCGTGGAGGAGTACGG V G F L G D E T R L P P A P G P G E S S H S I C P A

1387 AGTTGGTTTCTTGGAGACGAAACAGGCTCCCTCCCGCTCCAGGCCAGGAGAGTCTCCCATTCCTATCTGCCCTG

FIGURE 18AA

1464 Q V E L Q S L Y V D V H P K K G D L V Y S E I Q T 468
CCCAGGTGGAGCTTCAGTCGTTGTATGTTGATGTACACCCCAAAAGGGAGATTTGGTATACTCTGAGATCCAGACT
T Q L G E E E A N T S R T L L E D K D V S V Y S 494
1541 ACTCAGCTGGGAGAAGAAGAGGAAAGCTAATACCTCCAGACACTTCTAGAGATAAGGATGTCCTCAGTTGCTACTC
E V K T Q H P D N S A G K I S S K D E S * 515
1618 TGAGGTAAAGACACAAACACCCAGATACTCAGCTGGAAGATCAGCTCTAAGATGAAGAAAGTTAAGAGAATGAAA
1695 AGTTACGGGAACGTCCTACTCATGTGATTTCTCCCTTGTCCAAAGTCCCAGGCCAGTGCAGTCCCTTGGCGCACCTG
1772 GAATGATCAACTATCCAGCTTTCTAATTTCTCATGTGATATGCAATTCACCTCCAGGAATACTCATTCGTCTACT
1849 CTGATGTTGGGATGGAATGGCCTCTGAAGACTTCACTAAATGACCAGGATCCACAGTTAAGAGAAGACCCCTGTAG
1926 TATTTGCTGTGGGCTGACCTAATGCATTCCTAGGCTCTGCTTTAGAGAAGGGGGATAAAGAGAGAGAAGGACTGT
2003 TATGAAAAACAGAGCACAAATTTTGGTGAATTTGGGATTTTCAGAGATGAAAAAGACTGGGTGACCTGGATCTCTGC
2080 TTAATACATCTACAAACCATTTGTCTCACTGGAGACTCACTTGCATCAGTTTGTAACTGTGAGTGGCTGCACAGGCA
2157 CTGTGCAACAATGAAAAAGCCCTTCACTTCTGCTGAGAGATTAAGAAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
2234 CCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAGAGAGGACATCAGAAGAGCTGGAGATGCAAGCTCTAGGCTGC
2311 GCTTCCAAAAGCAAAATGATAATTATGTTAATGTCATTTAGTGACAAAAGATTTGCAACATTAGAGAAAAAGAGACACAAA
2388 TATAAAATTAATAAACTTAAGTACCAACTCCAAAACCTAAATTTGAACCTTAAATATTAGTATAAACTCATAATAAA
• CTCTGCCTTTTAAATAAAAAAATAAAAAAATAAAAAA

IRTA1 cDNA and protein sequence

[illegible]

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FIGURE 18B-1A

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1361 GCGTAGGTCGGCCAACTCTGCAGGAGGTGGCCATCAGCTTCTCTCTGCTGACGAGCATTTCAGGAACTACTACTGCA 475
      A D N G F G P Q R S K A V S L S I T V P V S H P V L
1441 CAGCTGACAAATGGCTTTGGCCCCCAGCGAGTAAGCGGTGAGCCTCTCCATCACTGTCCCTGTGTCTCATCCTGTCTCTC
      T L S S A E A L T F E G A T V T L H C E V Q R G S P Q 502
1521 ACCCTCAGCTCTGCTGAGGCCCTGACTTTTGAAGGAGCCTGTGACACTTCACTGTGAAGTCCAGAGAGGTTCCTCCACAC
      I L Y Q F Y H E D M P L W S S S T P S V G R V S F S F 529
1601 AATCCTATACCACTTTTATCATGAGGACATGCCCTGTGGAGCAGCTCAACACCCCTCTGTGGGAAGAGTGTCTCTTCAGCT
      S L T E G H S G N Y Y C T A D N G F G P Q R S E V V 555
1681 TCTCTCTGACTGAAGGACATTTCAGGGAATTACTACTGCACAGCTGACAATGGCTTTGGTCCCCCAGCGCAGTGAAGTGGTG

      S L F V T V P V S R P I L T L R V P R A Q A V V G D L 582
2A,2C1761 AGCCTTTTGTCACTGTCCAGTGTCTCGCCCCCATCTCACCTCAGGGTTCAGAGGCCCGGCTGTGGTGGGACCT
      G K C W V L A S H P P L A E F S L T H S F K 582
2B 1761 -----GGTAAGTGTGGGTCTTGCCAGTCACCCACCCCTGGCTGAGTTCTCTCTCACCCATTCTCTTTAA

      L E L H C E A P R G S P P I L Y W F Y H E D V T L G S 609
2A,2C1841 GCTGGAGCTTCACTGTGAGGCCCGGAGAGGCTCTCCCCCAATCCTGTACTGGTTTATCATGAGGATGTCACCCCTGGGGA
      N L F A L S S F L P * stop 592
2B 1841 AAATCTGTTTGCACTGTCCAGTTTCTCCCTTAATCAACTTAATCCCTTCTTGGCTTCTCTCAACTAAGTCTGGG

      S S A P S G G E A S F N L S L T A E H S G N Y S C E 635
2A,2C1921 GCAGCTCAGCCCCCTCTGGAGGAGAAGCTTCTTCAACCTCTCTCTGACTGCAGAACATTCTGGAAACTACTCATGTGAG
      GTTTCCGTACTCATAAGTCTCGGCTCAGCCAGACCCCTAAACAGCTCAGTAGATTTCCCGAGCTTTTACCAAATGAATT
2B 1921

      A N N G L V A Q H S D T I S L S V I V P V S R P I L T 662
2A,2C2001 GCCAACAAATGGCCTAGTGGCCCCAGCACAGTACACAAATATCACTCAGTGTATAGTTCAGTATCTCGTCCCATCCTCAC
      TATTTATTGTATTTTCTCTCATTCCTTTGATGTTCCCAACAGTACGCCCAATTTTCTTGTATGCACGGAGCGTGTCTCTACT
2B 2001

      F R A P R A Q A V V G D L L E L H C E A L R G S S P I 689
2A,2C2081 CTTCAGGGCTCCCAGGCCAGGCTGTGTGGGGACCTGTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCCTCCCCCAA
      TCTCTACTGACATTTACATATTAACCTTAGCTACAAGCACAGTCTTATAGATAAATATGGTCAAGACCTTAAATTTCTCCA
2B 2081
```


715

2721 AAAGCAGGGAGAAAGCCTGCTCTGACCCCGCAGGAGCGCTTCAGACTCGGACTCCCAAGAGCCACCTATCACAATGT
K A G R K P A S D P A R S P S D S D S Q E P T Y H N V 902

2721 GCCTCTACTCTTGAGTCTCTTTCAATTACTGGGGATGTAATGTTCTTTACATTTCCACATTAATAATCCTATGTTAAACGA

2721 CCCTTAATGCCAGTAGAATGTAAGCTTCATGAGAACAGAACTGCATCCATCTTGGTCTTCAACAATCCCTGTGCCTACT

2801	2C	P A W E E L Q P V Y T N A N P R G E N V Y S E V R I	929
2801	2A	ACCAGCCTGGGAAGAGCTGCAACCAGTGTACACTAATGCAAAATCCTAGAGGAGAAAATGTGGTTTACTCAGAAAGTACGGA	
2801	2B	AAAA CAGTGTGGCACACAGTAGGTCCTCAGTCAACATTGTGAATTTAGTGGACAGATGATGACAAGATGATAAGAGGGGA	
2881	2C	I Q E K K K H A V A S D P R H L R N K G S P I I Y S	955
2881	2B	TCATCCAAGAGAAAAAGAAACATGACAGTGGCCTCTGACCCCGGCATCTCAGGAACAAGGGTCCCTATCATCTACTCT TTTAAAAAATCATCTAGCAAGCCCAAGAGGAAAAAACAAGCTATTTTGAATGAAATACCAATTTGAAGCAGTA	
2961	2C	E X K V A S T P V S G S L F L A S S A P H R * stop	977
2961	2B	GAAGTTAAGGTGGCGTCAACCCCGGTTTCGGATCCCTGTCTTGGCTTCCTCAGCTCCTCAGATGAGTCCACACAGTC AGAAATAGATTGGATATCTTTGAAAAACCATTAATTGAATGAAGAACCAATTTGAGAAAAACAATACAGAAATGCAAAAGTAGAA	
3041	2C	TCTCCAACCTGCTGTTCAGCCTCTGCACCCCAAGTTCCCTTTGGGGAGAAAGCAGCATTTGAAGTGGGAAGATTTAGGCT	
3041	2B	AGATACAGAAAATAAAGGCAAAAGTTATAATATGAAATCAGACAATGGATTGTCTGTATCCAGTTATGTGGATAATTA	
3121	2C	GCCCCAGACCATATCTACTGGCCTTTGTTTCACATGTCTCTATCTCAGTCTGACCAGAAATGCAGGGCCCTGCTGGACTG	
3121	2B	AATGGAGACCTTCAGAAAATTGAACCGAAGAGTAAAAATGAAACTCAAAAATGTAGTAGAAATTTGTGGGAAGTAAAGAA	
3201	2C	TCACCTGTTTCCCAGTTAAAGCCCTGACTGGCAGGTTTTTTAATCCAGTGGCAAGGTGCTCCACATCCAGGGCCACAC	
3201	2B	ACTTGAATATGTAGATCAGAACATATATGTTGATGACGTTATTGACTTTGAGGTTAAAAATATATATGTGCTTATGAT	
3281	2C	ATCTCCTGATTCCTTAGTGGGCTTCAGCTGTGGTTGCTGTCTGAGTACTGCTCTCATCACACCCCCACAGAGGGGTC	
3281	2B	TATGGGGA AAAAAGCAGTCGCTCTCAGAAAAGAAAAACATCAAGTTAGTCTTAGACTTTGCACTGCACTCAGTACCAAAAG	
3361	2C	TTACCACAAAAGGAGAGTGGGCTTCAGGAGATGCCGGCTGGCTTAACAGCTCAGTGTCTCTAAACTCCGACACAG	
3441	2C	AGTTCTGCTTTGGGTGGATGCAATTTCTCAATTGTCAATCAGCCTGGTGGGCTACTGCACTGTGCTGCCAATATGGGACAG	
3521	2C	CACACAGCCTGTGCACATGGGACATGTGATGGGTCTCCCCACGGGGCTGCATTTTCAACATCTCTCCACCTGTCTCAAACT	
3601	2C	CTAAGGTCCGCACCTGACACCAAGGTAACTTCTCTCTGCTCATGTGTGCTCAGTCTTCTACCTGCCCCAAGTAAAGTGGCTTCA	
3681	2C	TACACCAAGTCCCGAAGTTCTTCCCATCTTACAGAAGTAACCCAGCAAGTCAAGGCCAGGAGGACCCAGGGTGCAGACA	
3761	2C	GAACACATACTGGAACACAGGAGGTGCTCAATTACTATTGACTGACTGACTGAATGAATGAATGAATGAAGGAAGAAAC	
3841	2C	TGTGGGTAAATCAAACTGGCATAAAAATCCAGTGCACCTCCCTAGGAAATCCGGGAGGTATCTGGCTTCTCCTAAGAAAAAC	
3921	2C	GAAGAGAAGGAGCTTGGATGAAGAAACTGTTTCAGCAAGAAGAGGGCTTCTTACACTTTTATGTGCTTGTGGATCACCT	
4001	2C	GAGGATCTGTGAAAAATACAGATACTGATTTCAGTGGGTCTGTGTAGAGCCTGAGACTGCCATTTCTAACATGTTTCCAGGGG	

FIGURE 18B-3

4081 ATGCTGATGCTGCTGGCCCTGGGACTGCACTGATGCACTGTAAGCCCTATAGTCTCAGCAGAGGCCCATGGAGAGGA
4161 ATGTGTGCTCTGGCTGCCAGGGCCCAACTCGGTTACACGGATCGTGTGCTCCTGGGCCAGCCCTTGGCCACAGCAC
4241 CACCAGCTGCTGTTGCTGAGAGAGCTTCTTCTGTGACATGTTGGCTTTCATCAGCCACCCCTGGGAAGCGGAAAGTAGC
4321 TGCCACTATCTTTGTTTCCCACTCAGGCCCTCACACTTCCCATGAAAGGGTGAATGATATTAACCTGAGCCCTCTCC
4401 ATTCAGAGTTGTTCTCCCATCTCTGAGCAATGGGATGTTCTGTTCCGCTTTTATGATATCCATCACATCTTATCTTGATC
4481 TTTGCTCCAGTGGATTGTACAGTGAATGACTTTTAAGCCCCACGGCCCTGAAATAAATCCTTCCAAGGCAATTGGAAGC
4561 TCACCTCCACTGAACCATGGCTTTTCATGCTTCCAAAGTGTACGGCCCTTGCCCAAGATAGACAGGGCTGACTCTGCTGCCC
4641 CAACCTTCAAGGAGGAACCCAGACACCTGAGACAGGAGCCTGTATGAGCCCAAGTGCAGCCTTGCAGAGGACAAAGCTG
4721 GAGGCATTTGTCACTACAGATATGCACTAATAATAGACGTGGAGCAAGAGAAATGCATTTCCACCGAGGCCGCTTTT
4801 TTAGGCCCTAGTTGAAAGTCAAGAGGACAGCAGCAAGCATAGGCTCAGGATTAAGAAAAAATCTGCTCACAGTCTGTT
4881 CTGGAGGTCACTACCCAAACAAGCTCACGGCCCTATGCAGTTCTGAGAAGGTGGAGGCCACCCAGGCTCAAAAGAGGAAATT
4961 TAGAATTTCTCATTTGGGAGAGTAAGGTACCCCCATCCAGATGATAACTGCACAGTGGCAGAACAACTCCACCCTAAT
5041 GTGGTGGACCCCATCCAGTCTGTTGAAGCCTGAATGTAAACAAAGGGCTTATCTTCTCAAGTAAGGGGAACTCCT
5121 GCTTTGGGCTGGGACATAAGTTTCTGCTTTCAGACGCAAACTGAAAAATGGCTCTTCTGGGTCTTTGAGCTTGTGGC
5201 ATATGGACTGAAAGAACTATGCTATTGGATCTCCTGGATCTCCAGCTTGCTGACTGCAGATCTTGAGATATGTCAGCCT
5281 CTACAGTCACAAGAGCTAATTCATTCTAATAAACCAATCTTTT

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FIGURE 18C-1

1 AGTGAAGGGTTTCCCATATGAAAAATACAGAAGAATTATTGTAATACTA
52 GCAATACACAACCTTGATATTTCTAGAGAACCCAGGCACAGTCTTGGAGAC
103 ATTACTCTGAGAGACTGCAGCTGATGGAAGATGAGCCCCCACTTCTAAAA
154 ATGTATCACTACCGGATTGAGATACAAACAGCATTTAGGAAGTCTCATC
205 TGAGTAGCAGCTTCTGCCCCCTCTTCTGGAGATAAGTCGGGCTTTTGGTG
256 AGACAGACTTTCCCAACCCCTCTGCCCGCGGTGCCCATGCTTCTGTGGCT
1 M L L W L
307 GCTGTGTGATCTCTGACTCTGGAAGAGAACAAATCAGGGTGGCCCCAAA
6 L L L I L T P G R E Q S G V A P K
358 AGCTGTACTTCTCTCAATCTCCATGGTCCACAGCCTTCAAAGGAGAAAA
23 A V L L L N P P W S T A F K G E K
409 AGTGGCTCTCATATGCAGCAGCATATCACATTCCTTAGCCCCAGGAGACAC
40 V A L I C S S I S H S L A Q G D T
460 ATATTGGTATCACGATGAGAAGTTGTTGAAAAATAAACATGACAAGATCCA
57 Y W Y H D E K L L K I K H D K I Q
511 AATTACAGAGCCTGGAATTTACCAATGTAGACCCGAGGATCCTCCCTCAG
74 I T E P G N Y Q C K T R G S S L S
562 TGATGCCGTGCATGTGGAATTTTCACCTGACTGGCTGATCCTGCAGGCTTT
91 D A V H V E F S P D W L I L Q A L
613 ACATCTGTCTTTGAGGAGACAAATGTCAATCTGAGATGTCAGGGGAAAGA
108 H P V F E G D N V I L R C Q G K D
664 CAACAAAAACACTCATCAAAAGGTTTACTACAAGGATGGAAAACAGCTTCC
125 N K N T H Q K V Y Y K D G K Q L P
715 TAATAGTTATAATTTAGAGAAGATCACAGTGAATTCAGTCTCCAGGGATAA
142 N S Y N L E K I T V N S V S R D N
766 TAGCAATATCATTTGACTGCTTATAGGAAGTTTACATACATGACATTGA
159 S K Y H C T A Y R K F Y I L D I E
817 AGTAACTTCAAAACCCCTAAATATCCAAGTTCAAGAGCTGTTTCTACATCC
176 V T S K P L N I Q V Q E L F L H P
868 TGTGCTGAGAGCCAGCTTCTCCACGCCCATAGAGGGGAGTCCCATGACCCCT
193 V L R A S S S T P I E G S P M T L
919 GACCTGTGAGACCCAGCTCTCTCCACAGAGCCAGATGTCCAGCTGCAATT
210 T C E T Q L S P Q R P D V Q L Q F
970 CTCCTCTTTCAGAGATAGCCAGACCCCTCGGATTGGGCTGGAGCAGGTCCCC
227 S L F R D S Q T L G L G W S R S P

FIGURE 18C-1A

1021 CAGACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTACTGGTG
244 R L Q I P A M W T E D S G S Y W C
1072 TGAGGTGGAGACAGTCACTCACAGCATCAAAAAAGGAGCCTGAGATCTCA
261 E V E T V T H S I K K R S L R S Q
1123 GATACGTGTACAGAGATCCCTGTGTCTAATGTGAATCTAGAGATCCGGCC
278 I R V Q R V P V S N V N L E I R P
1174 CACCGAGGGCAGCTGATTGAAGGAGAAAAATATGTCCTTATTGCTCAGT
295 T G G Q L I E G E N M V L I C S V
1225 AGCCCAGGGTTCAGGGACTGTCAATTCCTCTGGCACAAGGAAGAGAGT
312 A Q G S G T V T F S W H K E G R V
1276 AAGAAGCCTGGGTAGAAAGACCCAGCGTTCCTGTTGGCAGAGCTGCATGT
329 R S L G R K T Q R S L L A E L H V
1327 TCTCACCGTGAAGGAGAGTGATGCAGGGAGATCTACTGTGCAGCTGATAA
346 L T V K E S D A G R Y Y C A A D N
1378 CGTTCACAGCCCCATCCTCAGCACGCTGGATTCGAGTCCACCGTGAGATTCC
363 V H S P I L S T W I R V T V R I P
1429 GGTATCTCACCCCTGCTCCCTCACCTTCAGGGCTCCAGGGCCACACTGTGT
380 V S H P V L T F R A P R A H T V V
1480 GGGGGACCTGTGGAGCTTCACTGTGAGTCCCTGAGAGCTCTCCCCCGAT
397 G D L L E L H C E S L R G S P P I
1531 CCTGTACCGATTTATCATGAGGATGTCAACCTGGGGAACAGCTCAGCCCC
414 L Y R F Y H E D V T L G N S S A P
1582 CTCTGGAGGAGGAGCCTCCTTCAACCTCTCTCTGACTGCAGAACATCTGG
431 S G G G A S F N L S L T A E H S G
1633 AAACCTACTCCTGTGATGCAGACAATGGCCCTGGGGGCCACAGTCATGG
448 N Y S C D A D N G L G A Q H S H G
1684 AGTGAGTCTCAGGGTCACAGTTCGGGTGTCTCGCCCTCCTCACCCCTCAG
465 V S L R V T V P V S R P V L T L R
1735 GGCTCCCGGGCCAGGCTGTGTGGGGGACCTGTGGAGCTTCACTGTGA
483 A P G A Q A V V G D L L E L H C E
1786 GTCCCTGAGAGGCTCTCCCGATCCTGTACTGGTTTATCACGAGGATGA
499 S L R G S F P I L Y W F Y H E D D
1837 CACCTTGGGGAACATCTCGGCCACTCTGGAGGAGGGGCATCCTTCAACT
516 T L G N I S A H S G G A S F N L
1888 CTCTCTGACTACAGAACATTTCTGGAACACTACTCATGTGAGGCTGACAAATGG
533 S L T T E H S G N Y S C E A D N G

[illegible]

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FIGURE 18D-1

```
1  TGGTGACCAAGAGTACATCTCTTTTCAAATAGCTGGATTAGTCTCCTCATGC
1  M L
52  TGCTGTGGTCATGTGTCATCTTTTGATGCAGTCACTGAACAGGCAGATT
19  L W S L L V I F D A V T E Q A D S
103 CGCTGACCCCTTGTGGCCCTCTTCTGTCTTCGAAGGAGACAGCATCGTTC
36  L T L V A P S S V F E G D S I V L
154 TGAATGCCAGGGAGAACAGAACTGGAAATTCAGAAGATGGCTTACCATA
53  K C Q G E Q N W K I Q K M A Y H K
205 AGGATAACAAGAGTTATCTGTTTCAAAAAATTCAGATTTCCTTATCC
70  D N K E L S V F K K F S D F L I Q
256 AAAGTGCAGTTTAAAGTGACAGTGGTAACTATTCTGTAGTACCAAGGAC
87  S A V L S D S G N Y F C S T K G Q
307 AACTCTTTCTGGGATAAAACTTCAAATATAGTAAAGATAAAAGTCCAAG
104  L F L W D K T S N I V K I K V Q E
358 AGCTCTTTCAACGTCTGTGCTGACTGCCAGTCTCTCCAGCCCATCGAAG
121  L F Q R P V L T A S S F Q P I E G
409 GGGTCCAGTGAGCCTGAATGTGAGACCCGGCTCTCTCCACAGAGGTTGG
138  G P V S L K C E T R L S P Q R L D
460 ATGTTCAACTCCAGTTCTGCTTCTTCAGAGAAACACAGGTCTGGGGTCAG
155  V Q L Q F C F F R E N Q V L G S G
511 GCTGGACAGCTCTCGGAGCTCCAGATTTCGCCGTGTGGAGTGAAGACA
172  W S S S P E L Q I S A V W S E D T
562 CAGGTCTTACTGGTCAAGGCAGAAACGGTGACTCACAGGATCAGAAAC
189  G S Y W C K A E T V T H R I R K Q
613 AGAGCTCCAATCCAGATTACGTGCAGAGATCCCCATCTCTAATGTAA
206  S L Q S Q I H V Q R I P I S N V S
664 GCTTGAGATCCGGCCCCCGGGGACAGGTGACTGAAGGACAAAACCTGA
223  L E I R A P G G Q V T E G Q K L I
715 TCCTGTCTGTCTAGTGGCTGGGGGTACAGGAAATGTCACATTCTCCTGGT
240  L L C S V A G G T G N V T F S W Y
766 ACAGAGAGCCACAGGAACCATGTATGGGAAGAAACCCAGCGTTCCTGT
257  R E A T G T S M G K K T Q R S L S
817 CAGCAGAGCTGGAGATCCAGCTGTGAAGAGAGTGTATCCCGCAATATT
274  A E L E I P A V K E S D A G K Y Y
868 ACTGTAGAGCTGACAACGGCCATGTGCCTATCCAGAGCAAGGTGGTGAATA
291  C R A D N G H V P I Q S K V V N I
919 TCCCTGTGAGAAATCCAGTGTCTCGCCCTGCTCCTCACCCTCAGGTCTCTG
308  P V R I P V S R P V L T L R S P G
970 GGGCCAGGCTGAGTGGGACCTGTGGAGCTTCACTGTGAGGCCCTGA
325  A Q A A V G D L L E L H C E A L R
1021 GAGGCTCTCCCCCAATCTTGTACCAATTTTATCATGAGGATGTCACCCCTG
342  G S P P I L Y Q F Y H E D V T L G
```

FIGURE 18D-1A

1072 GGAACAGCTCGGCCCTCTGTGAGGAGGGGCTCCTTCAACCTCTCTTTGA
359 N S S A P S G G A S F N L S L T
1123 CTGCAGAACATTCTGGAACTACTCCTGTGAGGCCAACACGGCTGGGG
376 A E H S G N Y S C E A N N G L G A
1174 CCCAGTGCAGTGAGGCAGTCCAGTCTCCATCTCAGGACCTGATGGCTATA
393 Q C S E A V P V S I S G P D G Y R
1225 GAAGAGACCTCATGACAGTGGAGTTCTCTGGGACTGTTTGGTGTCTCTG
410 R D L M T A G V L W G L F G V L G
1276 GTTTCACCTGGTGTGCTTGTGCTGTTGATGCCCTTCCACAGATATCAG
427 F T G V A L L L Y A L F H K I S G
1327 GAGAAAGTTCTGCCACTAATGAACCCAGAGGGCTTCCAGGCCAAATCCTC
444 E S S A T N E P R G A S R P N P Q
1378 AAGAGTTCACCTATTCAAGCCCAACCCAGACATGGAGGAGCTGCAGCCAG
461 E F T Y S S P T P D M E E L Q P V
1429 TGTATGTCAATGTGGCTCTGTAGATGGATGTGGTTTATTTCTCAGGTCT
478 Y V N V G S V D V D V V Y S Q V W
1480 GGAGCATGCAGCAGCCAGAAAGCTCAGCAACATCAGGACACTTCTGGAGA
495 S M Q Q P E S S A N I R T L L E N
1531 ACAAGGACTCCCAAGTCATCTACTTCTGTGAAGAAATCAACACTTGG
512 K D S Q V I Y S S V K K S
1582 AGGAATCAGAAGGGAGATCAACAGCAAGGATGGGGCATCATTAAGACTTG
1633 CTATAAAACCTTATGAAAATGCTTGAGGCTTATCACCTGCCACAGCCAGAA
1684 CGTGCTCAGGAGGCACCTCCTGTCTATTTTCTCCTGATGATGTTCTTCT
1735 CCAATATCTTTTACCTATCAATATTCAATTGAACCTGCTGTACATCCAG
1786 ACACGTGCAAAATAATTTCTGTCTACCTTCTTTAAGCAATCAGTGTG
1837 TAAAGATTTGAGGGAAGAATGAATAAGAGATACAAAGGTCTCACCTTCATCT
1888 ACTGTGAAGTGATGAGAACAGGACTTGATAGTGGTGTATTAACCTTATTTAT
1939 GTGCTGTGGATACAGTTTGTCTAATAATTTTGTGAGAAATTTTGGCAATAT

FIGURE 18D-2

1990 GTTCATTGGGAATATTGGCCGTGAAATTTTCTTTCCACTGTGTCTCTGCCA
2041 GAATGTTTGTATCAGGCTGATGCTGGCTTCATAGAATGAGTTAGGCAGGAG
2092 CCCTTCCTCCTTGATTTTGGCATAGTTTCAGCAGGATGGTACCAGTTA
2143 TTCTTTCTGCATCTGTAGAAATTCAGCTATGAATCCATCTGGTCTAGGCT
2194 TTTGTGTTGGTTGGTAAGTTTCTCTCTCTCCCTGGTTCAATCTTGGGAGATTG
2245 ATTGGTCTAGGAGGGTTTCTCTCTCTCCCTCCAGATTTCTCTTTATGTGCA
2296 TGTGTTTCCAGGAATTTAGCCGTTTCTCCAGATTTCTCTTTATGTGCA
2347 TCGACTTGAGTGAACATTAATATATATGCACCTGGGAAACCAAAAATCTG
2398 TGTGACTTGCTTTATTTGCAGCATTTGTTTTATTTTGGTAGTCTGGAACTGA
2449 ACCTGCAATATCACCAAGTATGCATATAGTTGCAAAAATGTGATTTTGA
2500 CATAGTAAATAGAGTATTTGCAATAAACATATGATATTACITTTTGTAAAGTA
2551 TATAGATAAAAATGTAAATAATCTATATAAA

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FIGURE 18E-1

1 GAGGCATCTCTAGGTACCATCCCTGACCTGGTCCTC
37 ATGCTGCCGAGGCTGTGCTGTGATCTGTGCTCCACTCTGTGAA
M L P R L L L I C A P L C E
82 CCTGCCGAGCTGTTTTGATAGCCAGCCCTCCCATCCACAGAG
P A E L F L I A S P S H P T E
127 GGGAGCCCGAGTGACCCCTGACGTGTAAGATGCCCTTTCTACAGAT
G S P V T L T C K M P F L Q S
172 TCAGATGCCCCAGTCCAGTTCTGCTTTTTCAGAGACACCCGGGCC
S D A Q F Q F C F F R D T R A
217 TTGGGCCCCAGGCTGGAGCAGCTCCCCCAAGCTCCAGATCGCTGCC
L G P G W S S S P K L Q I A A
262 ATGTGAAAGAGACACAGGCTCATCTGTGCGAGGCACAGACA
M W K E D T G S Y W C E A Q T
307 ATGGCGTCCAAAGTCTTGAGGAGCAGGAGATCCCAGATAAATGTG
M A S K V L R S R R S Q I N V
352 CACAGGGTCCCTGCTGCTGATGTGAGCTTGAGAGACTCAGCCCCCA
H R V P V A D V S L E T Q P P
397 GGAGGACAGGTGATGGAGGGAGACAGGCTGCTCTCATCTGCTCA
G G Q V M E G D R L V L I C S
442 GTTGCTATGGGCACAGGAGACATCACCTTCCTTTGGTACAAAGGG
V A M G T G D I T F L W Y K G
487 GCTGTAGGTTAAACCTTCAGTCAAGACCCAGCGTTCACTGACA
A V G L N L Q S K T Q R S L T
532 GCAGAGTATGAGATTCCTCAGTGAGGAGAGTGATGCTGAGCAA
A E Y E I P S V R E S D A E Q
577 TATTACTGTAGCTGAAATGGCTATGGTCCCAGCCCCAGTGGG
Y Y C V A E N G Y G P S P S G
622 CTGGTGAGCATCACTGTCAGAATCCCGGTGTCTCGCCCCAATCCTC
L V S I T V R I P V S R P I L
667 ATGCTCAGGCTCCAGGCCAGGCTGCAGTGGAGGATGTGCTG
M L R A P R A Q A A V E D V L
712 GAGCTTCACTGTAGGCCCTGAGAGGCTCTCCTCCAATCCTGTAC
E L H C E A L R G S P P I L Y
757 TGGTTTTATCAGGAGGATATCACCTTGGGAGCAGGTGCGGCCCCC
W F Y H E D I T L G S R S A P
802 TCTGGAGGAGGAGCCTCCTTCAACCTTTCCCTGACTGAAGAACAT
S G G G A S F N L S L T E E H
847 TCTGAAACTACTCCTGTGAGGCCAACAATGGCCTGGGGGGCCAG
S G N Y S C E A N N G L G A Q
892 CGCAGTGAGGCGGTGACACTCAACTTCACAGTGCCTACTGGGGCC
R S E A V T L N F T V P T G A

FIGURE 18E-1A

937 AGAAGCAATCATCTTACCTCAGGAGTCATTGAGGGGCTGCTCAGC
R S N H L T S G V I E G L L S
982 ACCCTTGGTCCAGCCACCGTGGCTTATTATTGCTACGGCCTC
T L G P A T V A L L F C Y G L
1027 AAAAGAAAAATAGGAAGACGTTTCAGCCAGGGATCCACTCAGGAGC
K R K I G R R S A R D P L R S
1072 CTTCCAGCCCTTACCCCAAGAGTTCACCTACCTCAACTCACCT
L P S P L P Q E F T Y L N S P
1117 ACCCCAGGGCAGCTACAGCCTATATATGAAATGTGAATGTGTA
T P G Q L Q P I Y E N V N V V
1162 AGTGGGATGAGGTTTATTCACTGGCGTACTATATACCCGCGGAG
S G D E V Y S L A Y Y N Q P E
1207 CAGGAATCAGTAGCAGCAGAAACCCCTGGGACACATATGGAGGAC
Q E S V A A E T L G T H M E D
1252 AAGGTTTCCTTAGACATCTATTCCAGGCTGAGGAAAGCAACATT
K V S L D I Y S R L R K A N I
1297 ACAGATGTGGACTATGAAGATGCTATGTAA 1326
T D V D Y E D A M *
GGTT ATGGAAGATT CTGCTCTTTG
1351 AAAACCATCC ATGACCCCAA GCCTCAGGCC TGATATGTTT TTCAGAGATC
1401 CTGGGGCATT AGCTTTCCAG TATACCTCTT CTGGATGCCA TTCTCCATGG
1451 CACTATTCTT TCATCTACTG TGAAGTGAAG TTGGCGCAGC CCTGAAGAAA
1501 CTACCTAGGA GAACTAATAG ACACAGGAGT GACAGGGACT TTGTTATCAG
1551 AACCAGATTC CTGCCGGCTC CTTTGAANAAC AGGTCAATAT GTGCTCTTCT
1601 GTTTACAAGA GGAACAAGA TGGAAATAAAA GAAATTTGGA TCCTGGGTTG
1651 GAGGGACAGT GAAGCTTAGA GCACATGAAC TCAAGGTTAG TGAATCTGCA
1701 GGACTTCACA GAGAGAGCTG TGCCCATCAT TCAGTCCCAAG TGCTTTCTCT
1751 GCCCAGACAG CACAGAATC CAGCCCCGCT ACCTACATGG ATCATCGAGT
1801 TTCCACCTAA AATATGATTC TATTATTATT GAGTCACTGT TACCAAAATTA

FIGURE 18E-2

1851	GAACTAAAC	AAAGTTACAT	AAAAAGTTAT	TGTGACTCCA	CTTAATTTTA
1901	GTGACGTATT	TTTGTATATA	TAGGCCAAC	TATACCACAT	CCAAAATTAT
1951	GTATCTATTA	CAGCCCCTAG	AAGCTTTATA	AATACAGTGT	GTCTTCTTTT
2001	ATTCACAAA	TTTTTGAAAT	CGTGGTAATA	TGGTTGAAA	CCTGTATCTT
2051	AATTATTTT	TTTTTAAAT	GAGACAGGGT	CTCACTCTGT	CACTCAATCT
2101	GGAATGCAGT	GGCACATCT	TGCCCTCACTG	CAACGCTGC	CTCTCAGGCT
2151	CAAGCAAACC	TCTCACCTCA	GCCTGCTGAG	TAGCTGGGAC	TACAGGCACA
2201	TGCCACCAAA	CTTGGCCATT	TTTGTCTTA	CGTAGAGACA	AGATTTCAAC
2251	GTTTGGCCCA	GGCTGGTCTC	AAACTCCTGG	GCTCAAGCAA	TGTATTGAAT
2301	TTT				